

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 15:00:13 ; Search time 1459.44 Seconds
(without alignments)
7917.015 Million cell updates/sec

Title: US-08-709-662-1

Perfect score: 747
Sequence: 1 CTGCAAGACAGCTACCATGA.....AAAATAAATGTCATCAAC 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	747	100.0	747	9 AR059956	AR059956 Sequence
2	747	100.0	766	94 MAU41738	U41738 Mesocricetu
3	599.8	80.3	747	9 AR054141	AR054141 Sequence
4	586	78.4	586	97 HSU41737	U41737 Human pancr
5	536	71.8	558	9 AR038161	AR038161 Sequence
6	459.8	61.6	762	94 AB035204	AB035204 Mus muscu
7	451.8	60.5	788	94 AB028625	AB028625 Mus muscu
8	296.6	39.7	760	93 HSHIP	X68641 H.sapiens H

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9 296.6 39.7 784 97 HUMPARC D13510 Homo sapien
10 296.6 39.7 797 97 AR053327 AR053327 Sequence
11 296.6 39.7 797 97 S51768 PAP-H-pancr S51768
12 292.6 39.2 759 94 D63359 D63359 Mouse mRNA
13 287.2 38.4 798 9 AR076565 AR076565 Sequence
14 287.2 38.4 798 9 AR076565 AR076565 Sequence
15 287.2 38.4 798 9 HUMPARSEC M84337 Human pancr
16 286.8 38.4 781 9 AX004740 AX004740 Sequence
17 286.8 38.4 781 9 RATPARB M55149 Rat pancrea
18 285.4 38.2 729 95 RATPARC M98049 Rattus norv
19 285.2 38.2 779 95 S43715 S43715 reg-2-regen
20 279 37.3 793 9 AR076559 AR076559 Sequence
21 279 37.3 793 9 I13450 I13450 Sequence
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34 219.6 29.4 881 95 RATPARPIA L10229 Rat pancrea
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36 209.2 28.0 474 10 I13454 I13454 Sequence
37 168.4 22.5 1356 94 AB035211 AB035211 Mesocrice
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39 153.4 20.6 836 9 AX014211 AX014211 Sequence
40 153.4 20.5 537 94 AB035212 AB035212 Mus muscu
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42 145.4 19.5 598 89 AF172331 AF172331 Homo sapi
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ALIGNMENTS

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RESULT 1
AR059956 747 bp DNA PAT 29-SEP-1999
LOCUS AR059956
DEFINITION Sequence 1 from patent US 5840331.
ACCESSION AR059956
VERSION AR059956.1 GI:5986406
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 747)
AUTHORS Vink,A.I., Pittenger,G.L., Rafaeloff,R., Rosenberg,L. and
Duguid,W.P.
TITLE Ingap protein involved in pancreatic islet neogenesis
JOURNAL Patent: US 5840331-A 1 24-NOV-1998;
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source Location/Qualifiers
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/organism="unknown"
BASE COUNT 198 a 173 c 158 g 218 t
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Query Match 100.0%; Score 747; DB 9; Length 747;
 Best Local Similarity 100.0%; Pred. No. 7.8e-200;
 Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
MAU41738 766 bp mRNA ROD 08-OCT-1996
LOCUS MAU41738
DEFINITION Mesocricetus auratus pancreatic beta cell growth factor (INGAP)
ACCESSION U41738
VERSION U41738.1 GI:1514683
KEYWORDS
SOURCE golden hamster.
ORGANISM Mesocricetus auratus
REFERENCE 1 (bases 1 to 766)
AUTHORS Rafaeloff,R., Pittenger,G.L., Barlow,S.W., Qin,X.F., Yan,B.,
Rosenberg,L. and Vink,A.I.
TITLE Cloning and sequencing of the pancreatic beta cell growth factor
JOURNAL gene (INGAP) and its expression in islet neogenesis
REFERENCE 2 (bases 1 to 766)
AUTHORS Vink,A.I.
JOURNAL Direct Submission
SUBMITTED (01-DEC-1995) Aaron I. Vink, Eastern Virginia Medical
School, The Diabetes Institutes, 855 W. Brambleton Ave, Norfolk, VA
23510, USA

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Query Match 100.0%; Score 747; DB 9; Length 747;
 Best Local Similarity 100.0%; Pred. No. 7.8e-200;
 Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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BASE COUNT 207 a 179 c 160 g 220 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.8e-200;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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LOCUS Sequence 1 from patent US 5834590.
DEFINITION AR054141
ACCESSION AR054141
VERSION AR054141.1 GI:5979003
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1 (bases 1 to 747)
AUTHORS Vainik,A.I., Pittenger,G.L., Rafaeloff,R., Rosenberg,L. and
Duguid,W.P.
TITLE Ingap protein involved in pancreatic islet neogenesis
JOURNAL Patent: US 5834590-A 1 10-NOV-1998;
FEATURES Location/Qualifiers
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BASE COUNT 197 a 173 c 158 g 219 t
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Query Match 80.3%; Score 599.8; DB 9; Length 747;
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RESULT 4
LOCUS HSU41737 586 bp mRNA PRI 18-NOV-1997
DEFINITION Human pancreatic beta cell growth factor (INGAP) mRNA, complete cds.
ACCESSION U41737 GI:1514681
VERSION U41737.1
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Rafielloff, R., Piltenger, G.L., Barlow, S.W., Qin, X.F., Yan, B., Rosenberg, L., Duguid, W.P. and Vink, A.I.
TITLE Cloning and sequencing of the pancreatic islet neogenesis associated protein (INGAP) gene and its expression in islet neogenesis in hamsters
JOURNAL J. Clin. Invest. 99 (9), 2100-2109 (1997)
MEDLINE 97296198
REFERENCE 2 (bases 1 to 586)
AUTHORS Vink, A.I.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1995) Aaron I. Vink, Eastern Virginia Medical School, The Diabetes Institutes, 855 W. Brambleton Ave, Norfolk, VA 23510, USA
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/protein_id="AAB86497.1"
/db_xref="GI:1514682"
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LOCUS AR038161 558 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5804421.
ACCESSION AR038161
VERSION AR038161.1 GI:5956878
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 558)
AUTHORS Vink, A.I., Piltenger, G.L., Rafielloff, Phall, R. and Barlow, S.W.
TITLE High level of expression of ingap in bacterial and eukaryotic cells
JOURNAL Patent: US 5804421-A 4 08-SEP-1998;
FEATURES
source Location/Qualifiers
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BASE COUNT 149 a 130 c 124 g 155 t
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Best Local Similarity 99.1%; Pred. No. 2.4e-140;
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QY 626 AGCA 629
Db 543 AGCA 546

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RESULT 6
AB035204 762 bp mRNA ROD 29-APR-2000
LOCUS Mus musculus mRNA for Reg III delta, complete cds.
DEFINITION AB035204
ACCESSION AB035204.1 GI:6633973
VERSION Reg III delta.
KEYWORDS Mus musculus cDNA to mRNA.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE 1 (sites)
AUTHORS Abe,M., Naka,K., Akiyama,T., Shervani,N.J., Kobayashi,S.,
Tomioke-Kumagai,T., Ito,S., Takasawa,S. and Okamoto,H.
IDENTIFICATION of a novel Reg family gene, Reg IIdelta, and
mapping of all three types of Reg family gene in a 75 kilobase
mouse genomic region
JOURNAL Gene 246 (1-2), 111-122 (2000)
MEDLINE 20231736.
REFERENCE 2 (bases 1 to 762)
AUTHORS Okamoto,H., Takasawa,S. and Abe,M.
TITLE Direct Submission
JOURNAL Submitted (22-NOV-1999) to the DBJ/EMBL/GenBank databases. Shin
Takasawa, Tohoku University Graduate School of Medicine, Department
of Biochemistry; 2-1 Seiry-machi, Aoba-ku, Sendai, Miyagi
980-8575, Japan (E-mail:shinetsu@mail.cc.tohoku.ac.jp,
Tel:+81-22-717-8080, Fax:+81-22-717-8083)

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RESULT 7
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LOCUS Mus musculus INCApP mRNA for INCAp related protein, complete cds.
DEFINITION AB028625
ACCESSION AB028625.1 GI:7023940
VERSION INCApP; INCAp related protein.
KEYWORDS INCApP; INCAp related protein.
SOURCE Mus musculus (strain:BDJ-1) female duodenum mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Sasahara,K., Yamaoka,T., Moritani,M., Yoshimoto,K., Kuroda,Y. and
Itakura,M.
TITLE Molecular cloning and tissue-specific expression of a new member of

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RESULT 9
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DEFINITION Homo sapiens mRNA for PAP homologous protein, complete cds.
ACCESSION D13510
VERSION D13510.1 GI:285970
KEYWORDS PAP; pancreatitis-associated protein.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Itoh,T. and Teraoka,H.
TITLE Cloning and tissue-specific expression of cDNAs for the human and
JOURNAL mouse homologues of rat pancreatitis-associated protein (PAP)
MEDLINE Biochim. Biophys. Acta 1172 (1-2), 184-186 (1993)
93176807
COMMENT Submitted (27-OCT-1992) to DDBJ by:
Takako Itoh
Shionogi Research Laboratories
Shionogi & Co., Ltd.
Fukushima-ku, Osaka 553
Japan
phone: 06-458-5861 x376
Email: titohef1.lab.shionogi.co.jp
fax: 06-458-0987.
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Matches 431; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from patent US 5834214.
ACCESSION AR053327
VERSION AR053327.1 GI:5978189
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 797)

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VERSION	113456.1				
KEYWORDS	GI:910797				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 798)				
TITLE	Iovanna, J., Volker, K. and Dagorn, J.				
JOURNAL	Protein associated with acute pancreatitis agents for the screening				
FEATURES	of acute pancreatitis				
SOURCE	Patent: US 5436169-A 12-25-JUL-1995;				
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Db	575	AGGAGGGAGTCAACAGCCTGTGTGTTGGTGTGCAACATCATCATGAGGATGAGACACAGTGT	634
OY	608	GAGATCTACTCAGAGAGAGCAACACTGCGCTATACAGCCCAACACCAATTCCTTAT	663
Db	635	GAGAGCTACCTCTGAAGAGATATTTGCTTAATATTCCTCCCAACTGACCACTCAT	690

RESULT	15
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LOCUS	
DEFINITION	HUMANPANSECP 798 bp mRNA PRI 27-APR-1993
ACCESSION	
VERSION	M64337.1 GI:189600
KEYWORDS	pancreatitis-associated protein; secretory pancreatic protein.
SOURCE	Homo sapiens (Library: lambda gII) pancreas cDNA to mRNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS	Orelle,B., Keim,V., Meslotra,L., Dagorn,J. and Iovanna,J.L.
TITLE	Human pancreatitis associated protein. Messenger RNA cloning and expression in pancreatic diseases
JOURNAL	J. Clin. Invest. (1992) in press
FEATURES	Location/Qualifiers
SOURCE	I. 798

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7/2

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 14:59:33 ; Search time 1297.31 Seconds
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Title: US-08-709-662-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	456.2	61.1	758	192	AK019033	AK019033 Mus muscu
2	297.2	39.8	547	21	AI507901	AI507901 vp23g03.x
3	261.8	33.0	436	22	AI594831	AI594831 vp23g03.y
4	246.6	33.0	704	143	BE056837	BE056837 7k10d06.x
5	244	32.7	768	192	AK008446	AK008446 Mus muscu
6	242	32.7	768	192	AK008608	AK008608 Mus muscu
7	236.6	31.7	698	22	AI621017	AI621017 ts76a06.x
8	223.2	29.9	626	2	AA123026	AA123026 m8b2n07.r
9	223.2	29.9	373	12	AA822059	AA822059 vp23g03.x
10	222.2	29.7	570	13	AA871863	AA871863 vq41h11.r
11	221.6	29.7	579	13	AA871793	AA871793 vq41a12.r
12	220.4	29.5	606	122	AA916032	AA916032 EST347336
13	213	28.5	526	2	AA140246	AA140246 mq04f01.r
14	213	28.5	526	2	AA140246	AA140246 mq04f01.r
15	213	28.5	526	2	AA140246	AA140246 mq04f01.r
16	211.4	28.3	454	8	AA529218	AA529218 v133f12.r
17	207.8	27.8	442	163	BE136911	BE136911 ug57c06.y
18	207.8	27.8	475	14	AI007183	AI007183 ua72h01.r
19	207.8	27.8	475	163	BE138227	BE138227 ug50a06.y
20	206.4	27.6	462	163	BE135788	BE135788 ug55g04.y
21	206.4	27.6	470	163	BE135784	BE135784 ug55f12.y
22	205.4	27.5	485	189	W11664	W11664 ms92d06.r1
23	204.8	27.4	424	19	AI386122	AI386122 mq04f01.y
24	204.8	27.4	438	10	AA681777	AA681777 vt61c10.r
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26	203	27.2	461	163	BE135718	BE135718 ug54g06.y
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29	196.8	26.3	537	122	AA962460	AA962460 EST374533
30	194	26.0	521	13	AA871239	AA871239 vq32g10.r
31	188	25.2	364	156	C17743	C17743 C17743 Huma
32	187.8	25.1	482	11	AA124051	AA124051 mp98f05.r
33	187.2	25.1	429	2	AA124051	AA124051 mp98f05.r
34	186.6	25.0	475	1	AA059874	AA059874 m178b06.r
35	185.8	24.9	366	157	F14502	F14502 SSC1C03.FOR
36	185.6	24.8	475	13	AA869231	AA869231 vq49c07.r
37	185	24.6	578	11	AI027597	AI027597 ov99a02.x
38	183.6	24.6	645	111	AA084553	AA084553 wz26d11.x
39	181.8	24.3	426	13	AA871079	AA871079 vq44h01.r
40	181.8	24.3	624	118	AA583300	AA583300 ia03a07.x
41	179.6	24.0	513	13	AA871084	AA871084 vq44h06.r
42	179.4	24.0	584	12	AA851350	AA851350 EST194118
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44	176.2	23.6	641	164	BE200062	BE200062 ug57c07.x
45	171.8	23.0	304	109	AA056636	AA056636 AV056636

ALIGNMENTS

RESULT 1
LOCUS AK019033 758 bp mRNA HTC 08-FEB-2001
DEFINITION Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
enriched library, clone:1810046J24, full insert sequence.

ACCESSION AK019033
VERSION AK019033.1 GI:12859035

KEYWORDS CAP trapper.
MUS MUSCULUS (strain:C57BL/6J) 10 day old male pancreas cDNA to
mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
clone:1810046J24.

SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (sites)
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning

JOURNAL Methods Enzymol. 303, 19-44 (1999)
REFERENCE 2 (sites)
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE 3 (sites)
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M.,
Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T.,
Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T.,
Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Kashiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE 4 (sites)
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and
FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5 (bases 1 to 758)
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M.,
Hara, A., Hayatsu, N., Himoto, K., Hiroka, T., Horii, F.,
Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J.,
Kojima, Y., Konno, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T.,
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Sogabe, T., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission
JOURNAL Submitted (18-NOV-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp,
url: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
CDS

FEATURES

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tracer in a subtractive hybridization reaction. The driver
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Bento Soares and M. Fatima Bonaldo."
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DEFINITION Mus musculus adult male small intestine cDNA, RIKEN full-length
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ACCESSION  AK008446
VERSION     AK008446.1 GI:12842633
KEYWORDS    CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to
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ORGANISM
clone:2010205A03.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Carninci,P. and Hayashizaki,Y.
TITLE        High-efficiency full-length cDNA cloning
JOURNAL      Methods Enzymol. 303, 19-44 (1999)
AUTHORS      2 (sites)
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalisation and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL      2049374
MEDLINE
REFERENCE
AUTHORS      3 (sites)
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M.,
Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T.,
Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,
Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsui,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-Format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL      20530913
MEDLINE
REFERENCE
AUTHORS      4 (sites)
The RIKEN Genome Exploration Research Group Phase II Team and
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 768)
ADACHI,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Carninci,P., Fukuda,S., Furukoshi,Y., Furuno,M.,
Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,D.,
Kojima,Y., Konno,H., Koyama,K., Koyama,S., Kuribara,C., Matsuyama,T.,
Miyazaki,A., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Okazaki,Y.,
Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H.,
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Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A.,
Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
FEATURES
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DEFINITION	08-FEB-2001
ACCESSION	AK008608
VERSION	AK008608.1
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SOURCE	Cap trapper.
ORGANISM	Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to mRNA, clone:lib.RIKEN full-length enriched mouse cDNA library clone:2010322F10.
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	Carninci P. and Hayashizaki Y.
JOURNAL	High-efficiency full-length cDNA cloning Methods Enzymol. 303, 19-44 (1999)

REFERENCE	2 (sites)	
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	
MEDLINE	20499374	
REFERENCE	3 (sites)	
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoke,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M., Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsubiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.	
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	
MEDLINE	20530913	
REFERENCE	4 (sites)	
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.	
TITLE	Functional annotation of a full-length mouse cDNA collection	
JOURNAL	Nature 409, 685-690 (2001)	
REFERENCE	5 (bases 1 to 768)	
AUTHORS	Aadachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Atakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J., Kojima,Y., Konno,H., Koude,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toyota,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Yamatsu,M. and Hayashizaki,Y.	
TITLE	Direct Submission	
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)	
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.	
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	ACCESSION	t576a06.x1 NCI-GAP-GC6 Homo sapiens cDNA clone IMAGE:2237170 3'	
	VERSION	similar to G1:U5533_rnal PANCRAETITIS ASSOCIATED PROTEIN 1	
	KEYWORDS	PRECUSOR (HUMAN); mRNA sequence.	
	SOURCE	A1621017 GI:4630143	
	ORGANISM	Homo sapiens	
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
	TITLE	NCI-GAP http://www.ncbi.nlm.nih.gov/ncigap.	
	JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	COMMENT	Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapsb@remail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonalao, Ph.D. cDNA library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www.bio.lnl.gov/bdrip/image/image.html Insert Length: 872 Std Error: 0.00 Seq primer: -40UP from Glbpco High quality sequence stop: 457 POLYA-No.	
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	BASE COUNT	187 a 169 c 169 g 170 t 3 others	
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	Query Match	31.7%; Score 236.6; DB 22; Length 698;	
	Batches Similarity	64.4%; Pred. No.2.4e-60;	
	Matches 367; Conservative	0; Mismatches 202; Indels 1; Gaps 1;	
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Dy	144	GCTCTGTAAGCCTATGAGGCTCTATTGCTATTCATCGATGATTTTGATACCACAGACTGGTCT 202	
Dy	631	GCTCCAAAGGCTATGAGGCTCCCNCTGCTATGCTGCTGTTTNTGTACCAAAATTCGGAATG 572	
Dy	203	AATGAGAACTATCTGCGAATGATGATTTTCACAGACACCTGCAGATTTCTCTCAGTACT 262	
Dy	571	GATGCAATCTGCGCTGCGCAAGAGGCGCCCTCTGGAAAAGGGTGTCTGCTCAGTGGG 512	

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Db	511		452
OY	323	TGGATTGGACTGCCAATGATCCCTCACATGGTACACTACCCACGAAAGTGATGGAAGTG	382
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Db	331	CCTGGCCACTGTGGAGGCTGTCAAGAAACACAGATTTTCTAAGTGGAAAATTTAAAC	272
OY	503	TGTGAAATGAGCTTCCCTATATCTGCAAAATTCAGAGTCTAGGAGCATTTCTAATTCAC	562
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OY	623	AAGAGCAAGCTCTGCCTACACACCACAC	652
Db	151		122
RESULT	9		
LOCUS	AA123026		
DEFINITION	mp82ph07.r1 Soares thymus_2NBWT Mus musculus cDNA clone IMAGE:575772 5' similar to gb:U15533.fml PANCREATIC IS ASSOCIATED PROTEIN 1 PREDUCOR (HUMAN) : gb:D13509 Mouse mRNA for PAP homologous protein (MUSE);, mRNA sequence.		
ACCESSION	AA123026		
VERSION	AA123026.1		
KEYWORDS	GI:1681077		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 626) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellensberg,K., Steptoe,W., Tan,F., Underwood,K., Moore,B., Reisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.		
JOURNAL	The WashU-HMI Mouse EST Project		
COMMENT	Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. MGI:350421 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 495. Location/Qualifiers 1..626 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:575773" /clone_lib="Soares_thymus_2NBWT" /sex="male" /tissue_type="Thymus"		
FEATURES			
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		5' similar to gb:U15533_rnal PANCREATITIS ASSOCIATED PROTEIN 1				
		PRCURSOR (HUMAN) : gb:U13509 Mouse mRNA for PAP homologous protein				
		(MUSE) : mRNA sequence.				
ACCESSION		AA140246				
VERSION		AA140246.1	GI:1702682			
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SOURCE		house mouse.				
ORGANISM		Mus musculus				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS		1 (bases 1 to 526)				
		Marra,M., Hillier,D., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,				
		Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,				
		Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,				
		Thising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and				
		Waterston,R.				
TITLE		The WashU-HHMI Mouse EST Project				
JOURNAL		Unpublished (1996)				
COMMENT		Contact: Marra M/Mouse EST Project				
		WashU-HHMI Mouse EST Project				
		Washington University School of Medicine				
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
		Tel: 314 286 1800				
		Fax: 314 286 1800				
		Email: mouseest@watson.wustl.edu				
		This clone is available royalty-free through LLNL ; contact the				
		IMAGE Consortium (info@image.llnl.gov) for further information.				
		MG1:352401				
		Seq primer: -28M13 rev2 from Amersham				
		High quality sequence stop: 491.				
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		3']; double-stranded cDNA was ligated to Eco RI adaptors				
		(Pharmacia), digested with Not I and cloned into the Not I				
		and Eco RI sites of the modified pF7T3 vector. RNA				
		provided by Dr. Bertrand Jordan. Library went through two				
		rounds of normalization, and was constructed by Bento				
		Soares and M.Fatima Bonaldo."				
BASE COUNT		130 a 130 c 129 g 137 t				
ORIGIN						
		Query Match 28.5%; Score 213; DB 2; Length 526;				
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LOCUS	AKO08470	659 bp	mRNA HNC 08-FEB-2001
DEFINITION	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010207102, full insert sequence.		
ACCESSION	AKO08470		
VERSION	AKO08470.1	GI:12842670	
KEYWORDS	CAP trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to mRNA, clone:lib.RIKEN full-length enriched mouse cDNA library chrNA; clone:2010207102.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci,P. and Hayashizaki,Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Methods Enzymol. 303, 19-44 (1999)		
REFERENCE			
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
REFERENCE			
AUTHORS	20499374		
	3 (sites)		
	Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishik,K., Kitsunai,T., Tashiro,H., Itoh,M., Kituchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwakagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Itawo,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
REFERENCE			
AUTHORS	20530913		
	4 (sites)		
	The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE			
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Araki,A., Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayashi,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Itawa,M., Kato,H., Kawai,J.,		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 15:33:08 ; Search time 70.53 Seconds
(without alignments)
2005.039 Million cell updates/sec

Title: US-08-709-662-1

Perfect score: 747
1 CTGCAAGACAGCTACCAATCA.....AAAATAAATGTCATCAAC 747

Scoring table: IDENTITY_NUC
Gapox 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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6: /cgnl_7/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

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4	536	71.8	558	1	US-08-909-725-4
5	304.8	40.8	762	2	US-08-822-261-2
6	296.6	39.7	797	2	US-08-464-637-1
7	296.6	39.7	797	2	US-08-822-261-5
8	287.2	38.4	798	1	US-07-778-156-12
9	287.2	38.4	798	2	US-08-822-261-6
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24	102	13.7	378	2	US-08-340-426D-16
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31	46.6	6.2	140	1	US-08-518-878B-8	Sequence 8, Appl
32	46.6	6.2	140	1	US-08-294-522B-8	Sequence 8, Appl
33	46.6	6.2	140	2	US-08-807-861A-8	Sequence 8, Appl
34	46.6	6.2	140	2	US-08-470-868A-8	Sequence 8, Appl
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45	38.8	5.2	260	5	PCT-US95-17111A-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-08-709-662-1
Sequence 1, Application US/08709662
Patent No. 5840531
GENERAL INFORMATION:
APPLICANT: Vink, Aaron I.
APPLICANT: Piltenger, Gary L.
APPLICANT: Rosenlof, Ronit
APPLICANT: Ratselberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570,59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cricetus
FEATURE:
NAME/KEY: CDS
LOCATION: 20..541

US-08-709-662-1

Query Match 100.0%; Score 747; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 2,2e-236;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGCAAGACAGTACCTGATGCTTCCATGACCCCTGCTAGAGATGCTGATGCTGCT 60
QY 61 TTCTGCGCTGATGCTTCTCTTCTTGGTGAAGTGAAGAAATCTCAAAAGAACTGCTTC 120
   |||||||
DB 61 TTCTGCGCTGATGCTTCTCTTCTTGGTGAAGTGAAGAAATCTCAAAAGAACTGCTTC 120
QY 121 TTACGATATACCTGCTGCTCAAGGCTGTAGCCTATGGCTCTATTGCTATTCTGAT 180
   |||||||
DB 121 TTACGATATACCTGCTGCTCAAGGCTGTAGCCTATGGCTCTATTGCTATTCTGAT 180
QY 181 TTGATATACACAGACCTGCTGCTAATGACAACTATCCTGACAGATGCTTCTGAGACA 240
   |||||||
DB 181 TTGATATACACAGACCTGCTGCTAATGACAACTATCCTGACAGATGCTTCTGAGACA 240
QY 241 CTTGGCATTTCTCTCAGTACTGCTGAATTAACCTTGTCTCTCCCTTGTGAAGAACAG 300
   |||||||
DB 241 CTTGGCATTTCTCTCAGTACTGCTGAATTAACCTTGTCTCTCCCTTGTGAAGAACAG 300
QY 301 TTGAGCGGCTTACAGTACATCTGATGATGACTGCATGATCCTCAGATGCTACCTACC 360
   |||||||
DB 301 TTGAGCGGCTTACAGTACATCTGATGATGACTGCATGATCCTCAGATGCTACCTACC 360
QY 361 CAACGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
   |||||||
DB 361 CAACGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
QY 421 GAACCCCTATTGCTGCTGACCGGTGTTATGTGAGTTTGTCTGAGAATTCAGGTTT 480
   |||||||
DB 421 GAACCCCTATTGCTGCTGACCGGTGTTATGTGAGTTTGTCTGAGAATTCAGGTTT 480
QY 481 TCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 540
   |||||||
DB 481 TCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 540
QY 541 CTGAGCGAGTCTTAATTTCAACAGCTTGAAGAAATATATATGAAGCTCACATGAGCAAG 600
   |||||||
DB 541 CTGAGCGAGTCTTAATTTCAACAGCTTGAAGAAATATATATGAAGCTCACATGAGCAAG 600
QY 601 CAAGTATGAGGATTCACCTCAGGAAGCAAGCTCTGCTACACACCACCAATTCCTT 660
   |||||||
DB 601 CAAGTATGAGGATTCACCTCAGGAAGCAAGCTCTGCTACACACCACCAATTCCTT 660
QY 661 TATATATCTCTGCTGCTTCTTCTATCATGATATCTTGTGCTGTAACCTTAAAGCTC 720
   |||||||
DB 661 TATATATCTCTGCTGCTTCTTCTATCATGATATCTTGTGCTGTAACCTTAAAGCTC 720
QY 721 AGAGAACAAATAAATATATATATATATATATATATATATATATATATATATATAT 747
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DB 721 AGAGAACAAATAAATATATATATATATATATATATATATATATATATATATATAT 747
```

RESULT 2

US-08-401-530A-1

; Sequence 1, Application US/08401530A

; Patent No. 5834590

; GENERAL INFORMATION:

; APPLICANT: Vinik, Aaron I.

; APPLICANT: Piltenger, Gary L.

; APPLICANT: Rafaeloff, Ronit

; APPLICANT: Rosenberg, Lawrence

; APPLICANT: Duguid, William P.

; TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC

; TITLE OF INVENTION: ISLET NEOGENESIS

; NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti

STREET: 1001 G Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: US

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/401,530A

FILING DATE: 22-FEB-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 00570.48743

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 747 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Cricetulus

FEATURE:

NAME/KEY: CDS

LOCATION: 20..541

US-08-401-530A-1

Query Match 80.3%; Score 599.8; DB 2; Length 747;
Best Local Similarity 87.7%; Pred. No. 6.7e-188;
Matches 655; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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QY 1 CTGCAAGACAGTACCTGATGCTTCCATGACCCCTGCTAGAGATGCTGATGCTGCT 60
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DB 1 CTGCAAGACAGTACCTGATGCTTCCATGACCCCTGCTAGAGATGCTGATGCTGCT 60
QY 61 TTCTGCGCTGATGCTTCTCTTCTTGGTGAAGTGAAGAAATCTCAAAAGAACTGCTTC 120
   |||||||
DB 61 TTCTGCGCTGATGCTTCTCTTCTTGGTGAAGTGAAGAAATCTCAAAAGAACTGCTTC 120
QY 121 TTACGATATACCTGCTGCTCAAGGCTGTAGCCTATGGCTCTATTGCTATTCTGAT 180
   |||||||
DB 121 TTACGATATACCTGCTGCTCAAGGCTGTAGCCTATGGCTCTATTGCTATTCTGAT 180
QY 181 TTGATATACACAGACCTGCTGCTAATGACAACTATCCTGACAGATGCTTCTGAGACA 240
   |||||||
DB 181 TTGATATACACAGACCTGCTGCTAATGACAACTATCCTGACAGATGCTTCTGAGACA 240
QY 241 CTTGGCATTTCTCTCAGTACTGCTGAATTAACCTTGTCTCTCCCTTGTGAAGAACAG 300
   |||||||
DB 241 CTTGGCATTTCTCTCAGTACTGCTGAATTAACCTTGTCTCTCCCTTGTGAAGAACAG 300
QY 301 TTGAGCGGCTTACAGTACATCTGATGATGACTGCATGATCCTCAGATGCTACCTACC 360
   |||||||
DB 301 TTGAGCGGCTTACAGTACATCTGATGATGACTGCATGATCCTCAGATGCTACCTACC 360
QY 361 CAACGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
   |||||||
DB 361 CAACGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
QY 421 GAACCCCTATTGCTGCTGACCGGTGTTATGTGAGTTTGTCTGAGAATTCAGGTTT 480
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Db	421	GAACCCCTCTCTCTGCTGACCGTGTTATTTGGCAGTTTGTGTCTCAGAAATCAGGTTT	480
Qy	481	TCAGAGTGGCAGAGATTTTAAATTGTGAAAAATGAGCTTCCTATATCTGCAAAATTCAGGT	540
Db	481	TCAGAGTGGCAGAGATTTTAAATTGTGAAAAATGAGCTTCCTATATCTGCAAAATTCAGGT	540
Qy	541	CTAGGGCAGTCTCAATTTGCAACACCTTGAAAAATTTATGAAAGTCACATGACGACAAAG	600
Db	541	CTAGGGCAGTCTCAATTTGCAACACCTTGAAAAATTTATGAAAGTCACATGACGACAAAG	600
Qy	601	CAAGTATGAGGATTCACGTCAGGAGACCAAGCTCTGGCTACACACCACCAATTCCT	660
Db	601	TTATATCATCTCTGCTGTTTTTCTTGAAATTTATATGAAGTCACATGAGCAAGGAGC	660
Qy	661	TATATCATCTCTGCTGTTTTTCTATCAGTATATTTCTGTGGCTGTAACTTAAAGCTC	720
Db	661	AAGTATGAGGATTCACGTCAGGATTCAGTATATTTCTGTGGCTGTAACTTAAAGCTC	720
Qy	721	AGAGACAAAAATAAATGTCATCAAC	747
Db	721	AGAGACAAAAATAAATGTCATCAAC	747

	RESULT	3	
	US-09-146-969-3		
	; Sequence 3, Application US/09146969		
	; Patent No. 6228585		
	; GENERAL INFORMATION:		
	; APPLICANT: Dieckgraebe, Brian K.		
	; TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury		
	; FILE REFERENCE: 04255,75314		
	; CURRENT APPLICATION NUMBER: US/09/146,969		
	; NUMBER OF SEQ ID NOS: 5		
	; SOFTWARE: PatentIn Ver. 2.0		
	; SEQ ID NO 3		
	; LENGTH: 586		
	; TYPE: DNA		
	; ORGANISM: Homo sapiens		
	US-09-146-969-3		
	Query Match	78.4%; Score 586; DB 4; Length 586;	
	Best Local Similarity	100.0%; Pident.No. 2, Ie-183;	
	Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	24 TTCCCATGACCCCTCGTAGATGTCTTGAGAGCCTCTTCCGCCCTGATGTTCCATTCT	83	
Db	1 ttcccataccctcgtatagagtgcttgyagtcgcttccgcctgaqtlcttcltt	60	
OY	84 GGGTGAAGGTGAAGAATCTCAAAAGAAACTGCCTTCTTCACGTATACTGTCCTAAG	143	
Db	61 gggtygaaggygaagaactcaaaagaacgcctcttccaagtataacctgcctaag	120	
OY	144 GCCTGTAGCCTATGGGTCTATTGCTATTTCACTGATTTTGATACACAGACCTGGTGA	203	
Db	121 gctcgtagcctatgyggtcatattgctatctaacgatlltgataccacagaccgtgcta	180	
OY	204 ATGCAACAATCTCCTGCCAGATGCAATTTCTACGACACACTGSCATTCTTCCAGTACTG	263	
Db	181 atcgacaactatccctgcagagatgcatlctcagacacctgcatlcttcltcagtlacy	240	
OY	264 GTGAATTAACCTGCTGTGCTGCCCTTGAGAAGAACAGTTTGAGCGGCTCACAGTACATCT	323	
Db	241 gtgaattaacctcgtgtccctccctcttgyaagaacaglttgyacggccaccaagtaacct	300	
OY	324 GGATTGACATCCATGATCCTCACATGGTACACTACCCCAAGGGAAGTGGATGAAGTGA	383	
Db	301 ggatttgacctcatgatctccctcacatggtlaactaccacaagggaagtgtgatggaagtga	360	
OY	384 GCAGTTCCAATGTGCTGACCTTTCTATAACTGGGAGAGAACCCCTCTATTGCTGCTGACC	443	

Db 361 gcaagttccaaatgctgcagccttataactcgggaggaacccctattgctgcagc 420
 Oy 444 GTGCTTATFTGTCAGATTTTGTCTCAGAAATCAGSTTTTCAGAACTGAGAGATTTTAA 503
 Db 421 gtggattatgtgcagcttctgtctcagaatacagttcttcagaagtggagagattta 480
 Oy 504 GTGAAATGACCTTCCTATATCTGCAAAATTCAAAGTCTAGGGCAGTCTTAATTTCA 563
 Db 481 gtgaaatgagctccctacatactgcgaatcaatcaagtgctggagcttcaattca 540
 Oy 564 GCTTGAATAATTTATGAAAGCTACACATGAGCAGAGCAACAGTATGA 609
 Db 541 gcttgaataatattatgaagctcaatgacaaagaaagcaagtatga 586

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RESULT 4
US-08-909-725-4
: Sequence 4, Application US/08909725
: Patent No. 5804421
: GENERAL INFORMATION:
: APPLICANT: Vinik, Aaron
: APPLICANT: Pittenger, Gary
: APPLICANT: Rafaeloff-Phall, Ronit
: APPLICANT: Barlow, Scott
: TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
: TITLE OF INVENTION: IN GAP IN BACTERIAL AND EUKARYOTIC CELLS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Witcoff, Ltd.
: STREET: 1001 G Street, N.W.
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20001
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/909,725
: FILING DATE: 12-AUG-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/741,096
: FILING DATE: 30-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Kagan, Sarah A
: REGISTRATION NUMBER: 32,145
: REFERENCE/DOCKET NUMBER: 0570.05173
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-508-9100
: TELEFAX: 202-508-9299
: TELEX: 97430 BMB UT
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 558 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-909-725-4

Query Match 71.8%; Score 536; DB 1; Length 558;
Best Local Similarity 99.1%; Pred. No. 5,9e-167;
Matches 539; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

0Y 86 GTGGAAGTGTGAAGATCTCAAAAGAACTGGCTTCTACGATTAACCTGTCTCAAGGC 145
Db 3 GCGGATCCCGAAGATCTCAAAAGAACTGGCTTCTTACGATTAACCTGTCTCAAGGC 62
Y 146 TCTGTAGCTTAATGGGCTCTATTGCTATTTCACGTATTTTGATACACAGACCTGGTCTAAT 205

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|||||
Db 63 TCTGTACGCTATGGGCTCTATGCTATTTACTGATTTTGATACACAGACTGGTCTAAT 122
QY 206 GCNAACATATCCGCCGAGATGATTTCTCAGAGACACTGGCATTTCTTCAGACTGCT 265
Db 123 GCAGACATATCCGCGAGATGATTTCTCAGAGACACTGGCATTTCTTCAGACTGCT 182
QY 266 GAAATTCAGTCTGCTCCCTCTGTGAAGAACAGTTTGAGCGGCTTACAGTACATCTGG 325
Db 183 GAAATTCAGTCTGCTCCCTCTGTGAAGAACAGTTTGAGCGGCTTACAGTACATCTGG 242
QY 326 ATTGAGACTCATGATGATCCCTCATGATGTACACTACCAACGAGTGGAGTGGAGC 385
Db 243 ATTGAGACTCATGATGATCCCTCATGATGTACACTACCAACGAGTGGAGTGGAGC 302
QY 386 AGTTCCCAATGCTGACCTCTTATTAAGTGGAGAGAACCCCTTATTTGCTGCACTG 445
Db 303 AGTTCCCAATGCTGACCTCTTATTAAGTGGAGAGAACCCCTTATTTGCTGCACTG 362
QY 446 GGTATTTGCTCAGTTTGTCTCAGAAATCAGGTTTTCAGAGTGGAGATTTTAAATGT 505
Db 363 GGTATTTGCTCAGTTTGTCTCAGAAATCAGGTTTTCAGAGTGGAGATTTTAAATGT 422
QY 506 GAAATGAGCTCCCTTATCTGCAATTCAGAGTCTAGGGCAGTTTAAATTTCAACAGC 565
Db 423 GAAATGAGCTCCCTTATCTGCAATTCAGAGTCTAGGGCAGTTTAAATTTCAACAGC 482
QY 566 TTGAAATATTTATGAGACTCATGATGAGCAAGAGCAAGATGTAGGATTCACATCAGAG 625
Db 483 TTGAAATATTTATGAGACTCATGATGAGCAAGAGCAAGATGTAGGATTCACATCAGAG 542
QY 626 AGCA 629
Db 543 AGCA 546

RESULT 5
US-08-822-261-2
; Sequence 2, Application US/08822261
; Patent No. 5935813
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,261
; FILING DATE: Filed Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0251 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ISLNOT01
; CLONE: 2072483
US-08-822-261-2

Query Match 40.8%; Score 304.8; DB 2; Length 762;
Best Local Similarity 67.1%; Pred. No. 9, 8e-91;
Matches 432; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 9 CAGTACCATGATGCTTCCCATACCCCTCTGTAGATGTTTGGATGCTTCTTCTGCC 68
Db 106 CAGACACTATGCTGCTCCCATGCGCTGCCAGTGTGCTGGATGCTGCTTCTGCC 165
QY 69 TGATGTTCCCTTCTGTGGGAGTGAAGATCTCAAAAGAAAGTCCCTTCTTACGTA 128
Db 166 TCAATTTCTCTGTCTCAGGTTCAAGTGAAGAAACCCAGAGACTGCTTCTCCACGA 225
QY 129 TAACTGTCTCTCAAGGCTGTGACCTATGGTCTCTATTGCTATTCTACATGATTTGATAC 188
Db 226 TCAGCTGTCCCAAGAGGCTCCCAAGGCTATGGCTCCCTCTATGCTTGTGTCAC 285
QY 189 CACAGACCTGCTTAATGCAAACTATCCTGCCAGATGATTTTCTCAGACACTGGCAT 248
Db 286 CAAATTCCTGGATGATGATGCAATCTGGCTTGCAGAGGCGCCCTTGCAAACTGGTGT 345
QY 249 TTCTTCTCAGTACTGCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 308
Db 346 CTGTGCTCAGTGGGCTGAGGAGATCCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 405
QY 309 CCTACGATACATCTGATTTGACCTCATGATCCCTCAGATGATGATGATGATGATGAT 368
Db 406 GCTACATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 465
QY 369 GTGATGAGAGTGGAGACATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 428
Db 466 ATGATGAGAGTGGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525
QY 429 CTATTCCTGCTGACCTGCTGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 488
Db 526 CCAACATCTTAAACCTGGCCTGCTGAGGCTGTGCAAGAACACAGATTTCTGAAT 585
QY 489 GGAGAGATTTTAATGTAATGAAATGAGCTTCCCTATATGCAAAATTCAGAGTCTAGGCA 548
Db 586 GGAAGATTTTAATGTAATGAAATGAGCTTCCCTATATGCAAAATTCAGAGTCTAGGCA 645
QY 549 GTTCTATTTTCAACAGCTTGAATTAATTAATGAGCTCAGATGACCAAGAGCAATATAG 608
Db 646 GTTGGAGATGACAGCTTCAAGCTTGGCGGCTGATCATGATGATGATGATGATGATGAT 705
QY 609 AGGATTCACCTCAGAGAGCAAGCTGCTGCTACACACCAACACC 652
Db 706 AAGACTCACCTTGAAGAGAAATTTCTCCCAAACTGCCCCCTTACC 749

RESULT 6
US-08-464-637-1
; Sequence 1, Application US/08464637
; Patent No. 5834214
; GENERAL INFORMATION:
; APPLICANT: Iovanna, Juan-Lucio
; APPLICANT: Dagorn, Jean-Charles
; APPLICANT: Keim, Volker
; APPLICANT: Sarles, Jacques
; TITLE OF INVENTION: Detection of Pancreatitis-Associated
; TITLE OF INVENTION: Protein for Diagnosis of Cystic Fibrosis or Pancreatic
; TITLE OF INVENTION: Disease (as amended).
; NUMBER OF SEQUENCES: 2


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Db 35 CAGACATATGCTGCTCCATGAGCCCGCCGACAGTATCTTGAGTCTGCTTCTGCC 94
QY 69 TGAATGCTCTTCTTGAGGAGTGAAGATCTCAAAAGAACTGCTTCTCAGCTA 128
Db 95 TCATGCTGCTGCTCAGGTTCAAGGTAAAGACCCGAGGAACTCCCTCTGCACGGA 134
QY 129 TAACTGCTCCTCAGGCTCTGATGCTATGAGGCTTATGCTATTCATTCAGTATTTGATAC 188
Db 155 TCCGCTGCTCCAAAGGCTCCAGGCTATGAGCTCCACTGCTATGCTGCTTTTGTGCAC 214
QY 189 CACAGACCTGCTCTATGACAACTATCCCTCCAGATGCACTTTCTCAGGACCTGGCAT 248
Db 215 CAAATTCCTGGAGAGATGATCTGCTCCGACAGAGCGCCCTCGGAAACCTGGTGT 274
QY 249 TCTCTCTCAGTACTGAGGAATTAACCTGCTGCTCCCTGCTGTAAGAAAGTTTGACGG 308
Db 275 CTGTGCTCAGTGGGCTGAGGAGATCCTTCTGCTGCTGCTGCTGAGAGCATGGTACA 334
QY 309 CCTACCAATACATCTGATTTGAGCTCCATGATCCCTCATATGTTACATCCCAACGAA 368
Db 335 GCTACTATATGCTGATTTGGGCTGCTCATGACCCACAGAGGACCGACCAATGAG 394
QY 369 GTGATGAGAGTGGAGAGCTTCAATGCTGCTGACCTTTAACTGGGAGAGAACCCCT 428
Db 395 AAGTGGGAGTGGAGAGTGAATGATGATTAATCTTGATGAGAGAAATCCCT 454
QY 429 CTAATGCTGCTGACCGTGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
Db 455 CCACCATCTACAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
QY 489 GGAGAGATTTTAAATGTAATGAAATGAGCTTCCATATCTGAAATTCAGAGTGTAGGCA 548
Db 515 GGAAGATTTTAACTGTAATGAGTGTACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
QY 549 GTCTATATTTCAACAGCTTGAATATATATGAGCTCAGTCACTGAGCAAGAGCAAGATG 608
Db 575 GGAGGAGAGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
QY 609 AGGATTCACCTCAGAGAGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Db 635 AGGACTCACCTCGAAGAGATATTCGCTTAATTCCTCCCACTGACCACTCAT 689

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RESULT 8
US-07-778-156-12
; Sequence 12, Application US/07778156
; Patent No. 5436169

GENERAL INFORMATION:
; APPLICANT: IOVANA, JUAN-LUCIO
; APPLICANT: KEIM, VOLKER
; APPLICANT: DAGORN, JEAN-CHARLES
; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
; TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,156
; FILING DATE: 19911219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Oblon, No. 5436169man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 354-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: pancreas
; US-07-778-156-12

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Query Match 38.4%; Score 287.2; DB 1; Length 798;
Best Local Similarity 65.9%; Pred. No. 6, 3e-85;
Matches 432; Conservative 0; Mismatches 223; Indels 1; Gaps 1;

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QY 9 CAGTACCATGATGCTTCCCATGACCTCTGATGATGCTTGTGATGCTTCTGCC 68
Db 35 CAGACATATATGCTGCTCCCATGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 94
QY 69 TGAATGCTCTTCTTGAGGAGTGAAGATCTCAAAAGAACTGCTTCTCAGCTA 128
Db 95 TCATGCTGCTGCTCAGGTTCAAGGTAAAGACCCGAGGAACTCCCTCTGCACGGA 154
QY 129 TAACTGCTCCTCAGGCTCTGATGCTATGAGGCTTATGCTATTCAGTATTTGATAC 188
Db 155 TCCGCTGCTCCAAAGGCTCCAGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214
QY 189 CACAGACTGCTGCTTAAATGAGAACTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248
Db 215 CAAATTCCTGGAGAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 274
QY 249 TCTCTCTCAGTACTGAGGAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 308
Db 275 CTGTGCTCAGTGGGCTGAGGAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 334
QY 309 CCTACCAATACATCTGATTTGAGCTCCATGATCCCTCATATGTTACATCCCAACGAA 368
Db 335 GCTACTATATGCTGATTTGGGCTGCTCATGACCCACAGAGGACCGACCAATGAG 394
QY 369 GTGATGAGAGTGGAGAGCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
Db 395 AAGTGGGAGTGGAGAGTGAATGATGATTAATCTTGATGAGAGAAATCCCT 454
QY 429 CTAATGCTGCTGACCGTGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
Db 455 CCACCATCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
QY 489 GGAGAGATTTTAAATGTAATGAAATGAGCTTCCATATCTGAAATTCAGAGTGTAGGCA 547
Db 515 GGAAGATTTTAACTGTAATGAGTGTACCTATCTGCAAGTCTGCTGCTGCTGCTGCTGCT 574
QY 549 GTTCTAAATTTCAACAGCTTGAATATATATGAGCTCAGTCACTGAGCAAGAGCAT 607
Db 575 AGGAGGAGAGTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 634
QY 608 GAGATTCACCTCAGAGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Db 635 GAGAGCTCACCTCGAAGAGATATATGCTTAATTCCTCCCACTGACCACTCAT 690

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RESULT 9
US-08-822-261-6
; Sequence 6, Application US/08822261
; Patent No. 5935813

Query Match 38.4%; Score 287.2; DB 2; Length 798;
Best Local Similarity 65.9%; Pred. No. 6.3e-85;
Matches 432; Conservative 0; Mismatches 223; Indels 1; Gaps 1;

QY 9 CAGGTACCATGATGCTTCCCATGACCTCTGTAGAGATGCTTGGATGCTGTTCCGCC 68
DB 35 CAGACATGCTCTCCCTCCATGAGCCCTGCCCCAGTATCTGTGATGCTGCTTCCGCC 94
QY 69 TGAATGCTCTTCTTGGTGGAGAGTGAAGATCTCAAAAAGAACTGCTTCCAGCTA 128
DB 95 TCATGCTGCTCTCTCAGGTTTAAAGTGAAGAACCCAGAGGAAGTCCCTCTGACAGGA 154
QY 129 TAACCTGCTCAAGGCTCTGTAGCTATGAGGCTTATGCTATTCATTCAGTATTTGATAC 188
DB 155 TCCCTGTCCCAAGGCTCCCAAGGCTATGCTCCACCTGATGCTGTTTGTTCAC 214
QY 189 CACGACCTGCTTAATGCAAACTATCCCTGACAGATGCTATTCAGAGACCTGGCAT 248
DB 215 CAAATCTCGACAGATGCAATCTGCTGCGAAGGCGCCCTGTGAAACCTGGGT 274
QY 249 TTCTTCTAGTACTGTGAATTAATCTTCTGCTCCCTGTAAGAACAGTTTGACGG 308
DB 275 CTGTCCTCAGTGGGCTGAGGATCTTCTGCTCTCCCTGTGAAGATGTTGTAACA 334
QY 309 CCAACAGTACATCTGATGAGTGGACTCATGATCCCTACATGATGTAACCCAGGAA 368
DB 335 GCTACTCATAGCTGTGATTTGGCTCATGACCCACAGAGGACCGAGCCAAATGAG 394
QY 369 GTGATGGAAGTGAAGACATGCTGACCTTCTATACCTGGAGAGAACCCCT 428
DB 395 AAGGTTGGAGTGAAGTGAAGTGAATGATGATTAATCTTGTGAGAGAAATCCCT 454
QY 429 CTATGCTGCTGACGCTGATTTATGAGTGTGCTCAAGAAATCAGGTTTTCAGAGT 488
DB 455 CCACCATCTCAAGCCCGGCGACTGTGCGAGCTGTGAGAGACAGATTTCTGAGGT 514
QY 489 GAGAGATTTTAAATGGAATGAGCTTCCCTATATCTGCAAA-TTCAAGTCTTAGGGC 547
DB 515 GGAAGATTTTAACTGATGAGTGTACCTATGCTGCTGCAAGGTACACTGACTACTGC 574
QY 548 AGTTCTAATTTCAACAGCTTGAATAATTTATGAAGCTCAGATGAGCAAGAGCAATAT 607
DB 575 AGGAGGAGAGTCAAGCAGCTGTGTTGTGTCATCATCATGAGGATGAGACAGCTGT 634
QY 608 GAGGATTCACCTGAGAGCAAGCTGCTGCTATACACACCAACCAATTCCTTAT 663
DB 635 GAGGACTCACCTTGAAGAGATATTTGCTTAATTTCCCAACCTGACCACTCAT 690

RESULT 11
US-09-146-969-2
; Sequence 2, Application US/09146969
; Patent No. 6228585
; GENERAL INFORMATION:
; APPLICANT: Dieckgraebe, Brian K.
; TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
; FILE REFERENCE: 04255.75314
; CURRENT APPLICATION NUMBER: US/09/146,969
; CURRENT FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-969-2

Query Match 38.4%; Score 287.2; DB 4; Length 798;
Best Local Similarity 65.9%; Pred. No. 6.3e-85;
Matches 432; Conservative 0; Mismatches 223; Indels 1; Gaps 1;

QY 9 CAGGTACCATGATGCTTCCCATGACCTCTGTAGAGATGCTTGGATGCTGTTCCGCC 68

DB 35 CAGACATGCTCTCCCTCCATGAGCCCTGCCCCAGTATCTGTGATGCTGCTTCCGCC 94
QY 69 TGAATGCTCTTCTTGGTGGAGAGTGAAGATCTCAAAAAGAACTGCTTCCAGCTA 128
DB 95 TCATGCTGCTCTCTCAGGTTTAAAGTGAAGAACCCAGAGGAAGTCCCTCTGACAGGA 154
QY 129 TAACCTGCTCAAGGCTCTGTAGCTATGAGGCTTATGCTATTCATTCAGTATTTGATAC 188
DB 155 TCCCTGTCCCAAGGCTCCCAAGGCTATGCTCCACCTGATGCTGTTTGTTCAC 214
QY 189 CACGACCTGCTTAATGCAAACTATCCCTGACAGATGCTATTCAGAGACCTGGCAT 248
DB 215 CAAATCTCGACAGATGCAATCTGCTGCGAAGGCGCCCTGTGAAACCTGGGT 274
QY 249 TTCTTCTAGTACTGTGAATTAATCTTCTGCTCCCTGTAAGAACAGTTTGACGG 308
DB 275 CTGTCCTCAGTGGGCTGAGGATCTTCTGCTCTCCCTGTGAAGATGTTGTAACA 334
QY 309 CCAACAGTACATCTGATGAGTGGACTCATGATCCCTACATGATGTAACCCAGGAA 368
DB 335 GCTACTCATAGCTGTGATTTGGCTCATGACCCACAGAGGACCGAGCCAAATGAG 394
QY 369 GTGATGGAAGTGAAGACATGCTGACCTTCTATACCTGGAGAGAACCCCT 428
DB 395 AAGGTTGGAGTGAAGTGAAGTGAATGATGATTAATCTTGTGAGAGAAATCCCT 454
QY 429 CTATGCTGCTGACGCTGATTTATGAGTGTGCTCAAGAAATCAGGTTTTCAGAGT 488
DB 455 CCACCATCTCAAGCCCGGCGACTGTGCGAGCTGTGAGAGACAGATTTCTGAGGT 514
QY 489 GAGAGATTTTAAATGGAATGAGCTTCCCTATATCTGCAAA-TTCAAGTCTTAGGGC 547
DB 515 GGAAGATTTTAACTGATGAGTGTACCTATGCTGCTGCAAGGTACACTGACTACTGC 574
QY 548 AGTTCTAATTTCAACAGCTTGAATAATTTATGAAGCTCAGATGAGCAAGAGCAATAT 607
DB 575 AGGAGGAGAGTCAAGCAGCTGTGTTGTGTCATCATCATGAGGATGAGACAGCTGT 634
QY 608 GAGGATTCACCTGAGAGCAAGCTGCTGCTATACACACCAACCAATTCCTTAT 663
DB 635 GAGGACTCACCTTGAAGAGATATTTGCTTAATTTCCCAACCTGACCACTCAT 690

RESULT 12
US-07-778-156-1
; Sequence 1, Application US/07778156
; Patent No. 5436169
; GENERAL INFORMATION:
; APPLICANT: IOVANNA, JUAN-LUCIO
; APPLICANT: KEIN, VOLKER
; APPLICANT: DAGORN, JEAN-CHARLES
; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
; TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCLELLAND, MAIER & NEUBADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19911219
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5436169man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: pancreas
FEATURES:
NAME/KEY: CDS
LOCATION: 62..613
US-07-778-156-1

Query Match 37.3%, Score 279; DB 1; Length 793;
Best Local Similarity 65.6%; Pred. No. 3.2e-82;
Matches 422; Conservative 0; Mismatches 220; Indels 1; Gaps 1;

OY 5 AAGAGGTACCATGATGCTTCCATGACCCCTCTAGATGCTTGGATGCTGCTTCC 64
DB 50 ATGAGATTAATATGTTGATGCTTGGCTCCAGTATGCTGATGCTGCTGCTCC 109
OY 65 TGCCATGATGCTTCTTCTTGGGTGAAGTGAAGTCTCAAAAGAACTGCTTCTCA 124
DB 110 TGCCATGATGCTTCTTCTTGGGTGAAGTGAAGTCTCAAAAGAACTGCTTCTCA 169
OY 125 CGTATACCTGCTCTCAAGCTCTGTAGCTTATGCTTATGCTTATGCTATTTG 184
DB 170 CGCATTAATGCTCCCAAGGCTCCAGGCAATATGCTCTACTGATGCTTCTGAG 229
OY 185 ATACCAAGACCTGCTTAATGCAACTATCTCCAGATGCTTCTCAGAGACCTG 244
DB 230 ATACCAAGACCTGCTTATGCAACTGCTCCAGAAAGACCTGAAAGACCTT 289
OY 245 GCAATTTCTTCTAGTCTGTAATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 290 GATATGCTGCTCAATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 349
OY 305 ACGGCTTACCAATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 364
DB 350 AACACCTACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 409
OY 365 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
DB 410 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
OY 425 CCCCTATTTGCTGCTGACCGTGTATTTGCTGCAAAATTAATTAATTAATTAAT 484
DB 470 CCATTTACTGCTTATGACCGGATTTCTGCTGACCTTCTCAAGATCTTCTGATTTCT 529
OY 485 AAGTGAGAGATTTTAAATTTGAAAAATG-AGCTTCCATATATCTCAAAATTAAT 543
DB 530 AGATGAGAGATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 589
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DB 590 AAATTAACAGACAGCAACAGCTTATTTGCTGCAAGACAGATCTGTCAGAGGGGCA 649
OY 604 GATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 646
DB 650 ATATGAAGACTTGGCTAGAAAAAGTATTTCTATCTACAGTCC 692

RESULT 13
US-08-422-166-1
Sequence 1, Application US/08422166
Patent No. 5959086
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, WAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5959086man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: pancreas
FEATURES:
NAME/KEY: CDS
LOCATION: 62..613
US-08-422-166-1

Query Match 37.3%, Score 279; DB 2; Length 793;
Best Local Similarity 65.6%; Pred. No. 3.2e-82;
Matches 422; Conservative 0; Mismatches 220; Indels 1; Gaps 1;

OY 5 AAGAGGTACCATGATGCTTCCATGACCCCTCTAGATGCTTGGATGCTGCTTCC 64
DB 50 ATGAGATTAATATGTTGATGCTTGGCTCCAGTATGCTGATGCTGCTGCTCC 109
OY 65 TGCCATGATGCTTCTTCTTGGGTGAAGTGAAGTCTCAAAAGAACTGCTTCTCA 124
DB 110 TGCCATGATGCTTCTTCTTGGGTGAAGTGAAGTCTCAAAAGAACTGCTTCTCA 169
OY 125 CGTATACCTGCTCTCAAGCTCTGTAGCTTATGCTTATGCTTATGCTATTTG 184
DB 170 CGCATTAATGCTCCCAAGGCTCCAGGCAATATGCTCTACTGATGCTTCTGAG 229
OY 185 ATACCAAGACCTGCTTAATGCAACTATCTCCAGATGCTTCTCAGAGACCTG 244


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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/422,166
: FILING DATE: 14-APR-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/778,156
: FILING DATE: 19-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Oblon, No. 5959086man F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 354-012-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703)521-4500
: TELEFAX: (703)486-2347
: TELEX: 248855 OPAT UR
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 522 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: TISSUE TYPE: pancreas
: US-08-422-166-4

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Job time: 3114 sec

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Query Match          34.2%; Score 255.6; DB 2; Length 522;
Best Local Similarity 68.3%; Pred. No. 1.3e-74;
Matches 354; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 17 ATGATGCTTCCCATGACCCCTGTGAGATGCTGATGCTGCTTCTGCTGATGCTTC 76
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Db 1 ATGCGCTCCCATGAGGCGCTGATGCTGATGCTGATGCTGCTTCTGCTGATGCTG 60

QY 77 CTTTCTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CTGCTCAAGGTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120

QY 137 CCTCAAGGCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CCCAAGGCTCCAGAGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 180

QY 197 TGGTCTATGACAGACTCTGCTGACAGATGCTGCTGACAGACTCTGCTGACAGACTCTGCT 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TGGACAGATGACAGATGCTGCTGACAGAGGCGCCCTGAGAACTGCTGCTGCTGCTC 240

QY 257 AGTACTGCTGAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 AGTGGGCTGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 317 TACATCTGATTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 376
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Db 301 TACGCTCTGATTTGGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

QY 377 AAGTGAAGCACTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
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Db 361 GAGTGAAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

QY 437 GCTGACCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
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Db 421 TCAAGCCCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

QY 497 TTTAATTTGAAATGAGCTTCCCTATATCTGCAATTT 534
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Db 481 TATACTGTAATGTGAGGTTAACCCTATGCTGCAAGT 518

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 15:35:18 ; Search time 104.73 Seconds
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Title: US-08-709-662-1

Perfect score: 747
Sequence: 1 CTGCAAGACAGTACCATGA.....AAAATAAATGTCATCAAC 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	100.0	747	17	AAT36612
2	586	78.4	586	21	AAZ99822
3	536	71.8	558	19	AAV46422
4	536	71.8	558	19	AAV40284
5	304.8	40.8	763	19	AAV58279
6	304.8	40.8	859	20	AAZ34271
7	304.8	40.8	859	21	AACT8569
8	286.6	39.7	797	15	AAO69201
9	296.6	39.7	940	21	AACT7777
10	291	39.0	756	19	AAV55234
11	287.2	38.4	798	12	AAQ14623

12	287.2	38.4	798	21	AAZ99821	CDNA sequence of h
13	286.8	38.4	781	20	AAZ26126	Reg-2 protein enco
14	286.8	38.4	781	21	AAZ75486	DNA encoding a rat
15	279	37.3	793	12	AAQ14621	Fragment S1 encod
16	260.8	34.9	528	15	AAO64172	Mouse PAP. Mus mu
17	258.2	34.6	528	15	AAO64171	Mouse PAP. Mus mu
18	255.6	34.2	522	12	AAQ14619	Fragment S3 from h
19	245.4	32.9	790	11	AAO05300	Bovine pancreatic
20	212.4	28.4	602	12	AAI16252	Human colon cancer
21	209.2	28.0	474	12	AAQ14620	Fragment S2 from r
22	182.4	24.4	461	21	AACT8317	Human cancer assoc
23	153.8	20.6	836	20	AAZ41387	Human normal pancer
24	153.8	20.6	845	21	AAZ99066	Human pancreatic c
25	145.4	19.5	800	22	AAZ75077	Human colon associ
26	145.4	19.5	843	21	AACT7946	Human cancer assoc
27	145.4	19.5	843	22	AAZ75090	Human colon associ
28	143.8	19.3	777	21	AAZ99820	CDNA sequence of h
29	141	18.9	749	9	AAZ81961	Sequence of rat re
30	137.8	18.4	495	10	AAZ91109	Human reg CDNA. H
31	137.8	18.4	498	9	AAZ81962	Sequence of reg ge
32	135	18.1	495	10	AAZ81181	Sequence of reg ge
33	134.6	18.0	495	10	AAZ91110	Rat reg CDNA. Rat
34	133.8	17.9	495	14	AAQ40477	MURK-1 coding reg
35	120.4	16.1	610	21	AAZ16224	Human colon cancer
36	118.2	15.8	441	11	AAQ05622	Sequence encoding
37	107.2	14.4	519	14	AAQ04078	MURK-2 coding reg
38	96.4	12.9	716	21	AAZ98838	Human pancreatic c
39	94	12.6	94	19	AAV46419	INGAP 5'-end CDNA
40	94	12.6	94	19	AAV30281	INGAP coding seque
41	92	12.3	622	21	AAZ16219	Human colon cancer
42	86.4	11.6	659	21	AAZ16314	Human colon cancer
43	83.6	11.2	277	21	AAZ10817	Human secreted pro
44	73.4	9.8	306	12	AAQ14622	Fragment encoding
45	63.4	8.5	568	21	AAZ9185	Human pancreatic c

ALIGNMENTS

RESULT 1	
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AC	AAT36612:
XX	XX
DT	18-APR-1997 (first entry)
XX	XX
DE	Hamster islet neogenesis associated protein gene.
XX	XX
KW	Hamster: islet neogenesis associated protein; INGAP; pancreas; endocrine;
KW	differentiation; pancreatic tissue; cellphane; duct epithelium; homology;
KW	pancreatic associated protein; open reading frame; liver; adenocarcinoma;
KW	beta-cell; regeneration; insulin; diabetes; mamal; ss.
XX	XX
OS	Cricetulus sp.
XX	XX
FH	Key
FT	CDS
FT	FT
XX	XX
PN	W09626215-A1.
XX	XX
PD	29-AUG-1996.
XX	XX
PE	12-FEB-1996; 96WO-US01528.
XX	XX
PR	07-NOV-1995; 95US-0006271.
XX	XX
PR	22-FEB-1995; 95US-0401350.
XX	XX
PA	(EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.
XX	XX

Location/Qualifiers
/*tag= a
/product= islet neogenesis associated protein

PI Duguid WP, Pittenger GL, Rafaeloff R, Rosenberg L:
 PI Vainik AI:
 DR WPI: 1996-402318/40.
 DR P-PSDB: AAR98525.
 XX
 PT Mammalian islet neo:genesis associated protein - isolated by
 PT stimulating mammalian pancreas by wrapping in cellopthane, for
 PT treatment of diabetes, etc
 XX
 PS Claim 13; Page 26; 50pp; English.
 XX
 CC This is the nucleotide sequence encoding the hamster islet neogenesis
 CC associated protein (INGAP). The gene is isolated from pancreatic cells
 CC which are induced to proliferate upon wrapping pancreatic tissue in
 CC cellopthane. Wrapping of the pancreas stimulate proliferation of new
 CC endocrine cells which appear from duct epithelium. The INGAP gene was
 CC isolated from a cDNA library constructed from mRNA purified from
 CC cellopthane wrapped hamster pancreas using a differential display method
 CC to compare genes expressed in cellopthane-wrapped and control pancreas.
 CC The gene contains an open reading frame which encodes a protein of 175
 CC amino acids. The protein has structural homology to the pancreatitis
 CC associated protein (PAP)/HIF family of genes which is associated with
 CC pancreatic or liver adenocarcinoma, and to the Reg/PSP/11thostaline
 CC (PSP = pancreatic stone protein) family of gene which has been shown to
 CC stimulate pancreatic beta-cell growth and may be involved in pancreatic
 CC islet regeneration. The protein can be used to stimulate islet cell
 CC proliferation in (non-)insulin dependent diabetic mammals.
 XX
 SQ Sequence 747 BP; 198 A; 173 C; 158 G; 218 T; 0 other;

Query Match 100.0%; Score 747; DB 17; Length 747;
 Best Local Similarity 100.0%; Pred. No. 1.8e-223;

Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGACAGGTACATGATGCTTCCATGACCTCTGTAGAGATGTTGATGCTGCT 60
 DB 1 ctgaaagacaggtacacatgctgctccacgacctctgtagagctgctgagctgct 60
 QY 61 TTCTGCTGATGTTCTTCTTCTTGGTGGAGAGAGATTCGAAGAAGCTGCTTC 120
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 QY 121 TTTCAGTATACCTGCTCTGAGGCTCTGAGCTATGCTGCTATGCTATGCTATG 180
 DB 121 ttacagataactgcttcttcttcttcttcttcttcttcttcttcttcttcttctt 180
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 DB 181 ttgatataccacagacctgctgcttcttcttcttcttcttcttcttcttcttctt 240
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 QY 301 TTTCAGGCTCTGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 DB 301 ttgagcgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 360
 QY 361 CAACGAGATGATGAGATGAGACAGCTTCAATGCTGAGCTTCTATATGCTGAGAG 420
 DB 361 caacgagatgagatgagatgagacagcttcaatgctgagcttctatatactgagag 420
 QY 421 GAACCCCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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DB 541 ctgagcgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 600
 QY 601 CAAGTATGAGGATTTCTACTGAGAGACAGCTTCTGCTTACACACCACTATTCCT 660
 DB 601 caagtatgagatgagatgagatgagacagcttcttcttcttcttcttcttcttctt 660
 QY 661 TATATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 DB 661 tatatacctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctt 720
 QY 721 AGAGAACAAAAATTAATGCTATCAAC 747
 DB 721 agagaaacaaaataaatgctacacac 747

RESULT 2

AA299822 standard; cDNA; 586 BP.
 ID AA299822 standard; cDNA; 586 BP.
 XX
 AC AA299822;
 DT 12-JUL-2000 (first entry)
 DE
 XX cDNA sequence of human pancreatic beta cell growth factor (INGAP).
 KW Human: pancreatic beta cell growth factor; INGAP: regenerating gene;
 KW REG gene: chronic mucosal injury; Hs.111244 polynucleotide;
 KW ulcerative colitis; Crohn's disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200014283-A2.
 XX
 PD 16-MAR-2000.
 XX
 PF 03-SEP-1999; 99WO-US20098.
 XX
 PR 04-SEP-1998; 98US-0146969.
 XX
 PA (UNIT) UNIV WASHINGTON.
 XX
 PI Dieckgraefe BK;
 XX
 DR WPI: 2000-257019/22.
 XX
 PT Diagnosing chronic mucosal injury such as ulcerative colitis and
 PT Crohn's disease comprises detecting expression levels of regenerating
 PT gene family and a gene represented by a Hs.111244 polynucleotide in a
 PT human body sample -
 XX
 PS Disclosure: Page 36; 42pp; English.
 XX
 CC The present sequence represents the cDNA sequence of human pancreatic
 CC beta cell growth factor (INGAP). The INGAP gene is part of the
 CC regenerating (REG) gene family. In normal circumstances, REG genes are
 CC regionally expressed in low amounts in the small bowel and pancreatic
 CC epithelium. However, they are strongly expressed in regions of the colon
 CC involved with chronic mucosal injury. The specification describes a
 CC method for diagnosing chronic mucosal injury by detecting expression
 CC levels of the REG gene family and a gene represented by a Hs.111244
 CC polynucleotide in a human body sample. The methods are useful for
 CC diagnosing chronic mucosal injury such as ulcerative colitis and Crohn's
 CC disease by detecting expression levels of the REG gene family and
 CC a gene represented by a Hs.111244 polynucleotide, respectively, in a
 CC human body sample.
 XX
 SQ Sequence 586 BP; 148 A; 132 C; 130 G; 176 T; 0 other;

Query Match 78.4%; Score 586; DB 21; Length 586;
 Best Local Similarity 100.0%; Pred. No. 3.2e-173;
 Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 24 TTCCATGACCCCTGTGAGAGATGCTTGAGATGCTTCCGCTGATGTTCTTCTT
Dd 1 ttccatgacctctgtgagatgcttggatgctgtcttcctgctgctgcttctt
QY 84 GGGTGGAGGCTGAGGAATCTCAAAAGAAACAGCTCTTCTTCACTAATACCTGCTCAAG
Dd 61 gggttggaggctggaagaatctcaaaagaacagctcttcttcagatatacctgcttccaa
QY 144 GCTGTAGACCTATGGGCTATGCTATGCTATTCAGATTTTGTATTCACAGACAGCTGCTGCTA
Dd 121 gctctgtagacctatgggctctatgctctatgcttcaacagatttgatccacaagaccggtctca
QY 204 ATGCAGACATATCCCTGCAGATGATTCATTCAGAGACACCTGGACATTTCTTCTCAGTACTG
Dd 181 atgcagacatctcctgcagatgctatcttcagagacacccctgagcttctctcagtaactg
QY 264 GTGAATTAATCCTTGTGCTCTCCTTGTGAAGAACAGTTTGACGCGCTACCACTGATCATCT
Dd 241 gtgaattaatccttgtgctctccttgtgaagaacagtttgacgagcctacacagtaactct
QY 324 GGATTTGACCTCATGATCCCTGCATGCTATCCATCCCAAGGAAGTGAAGTGAAGTGA
Dd 301 ggatttgacctcatgataccctcacacatggttacatccacaagagtggaagtga
QY 384 GCAGTTCATATGCTGCTGACCTTCTATTAAGTGGAGAGAACCCCTCTATTTGCTGCTGAC
Dd 361 gcagtccaatgctgctgacacctctctatactgagaggaagaaacctctcatgtgctgac
QY 444 GTGCTTATTTGTGCAATTTTGTCTCAGAAATCAGTTTTCAGAGTGGAGAGATTTTAATT
Dd 421 gtgctttatgtgcaattttgtctcagaatcaggttttcagaagatlgagagatttlaatt
QY 504 GTGAAATGACCTTCCCTATATCTGCAAAATTCAGAGTCTAGGCACTTCTAATTTCAACA
Dd 481 gtgaaatgaccttccctatactcgaatcgaaggtctagagcagttctaattcaaca
QY 564 GCTTGAATAATTTATGAAAGCTCAGATGACCAAGAGAGCAAGTATATGA
Dd 541 gcttgaataatttatgaaagctcacatgagcaagaagaaagtaactga
RESULT 3
AAV46422
ID AAV46422 standard; cDNA; 558 BP.
AC AAV46422;
Dd 18-NOV-1998 (first entry)
Dd 18-NOV-1998 (first entry)
DE INGAP PCR product cDNA.
XX
KW INGAP: islet neogenesis-associated protein; treatment; diabetes;
KW host cell; ss.
XX
OS Unknown.
XX
PN US5804421-A.
XX
PD 08-SEP-1998.
XX
PF 12-AUG-1997; 97US-0909725.
XX
PR 12-AUG-1997; 97US-0909725.
XX
PR 30-OCT-1996; 96US-0741096.
XX
PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.
XX
PI Barlow SM, Pittenger GL, Rafaeloff-Phail R, Vinik AI;
XX
PI WPI; 1998-505656/43.
XX
PT Expression of islet neogenesis-associated protein - from recombinant
```

```
PT construct lacking signal peptide, useful in the treatment of
PT diabetes
XX
XX Claim 16; Column 14; 14pp: English.
PS
XX
CC This cDNA sequence is an amplified PCR product of the islet
CC neogenesis-associated protein (INGAP) which is used in the construction
CC of a recombinant construct having a coding sequence lacking a signal
CC sequence and is operably linked to transcription and translation
CC initiation sites. This construct in a host cell is useful for producing
CC recombinant mature INGAP, which is useful in the treatment of diabetes.
CC High levels of INGAP expression can be achieved in bacterial and
CC eukaryotic cells by removing the signal peptide as it is possibly
CC toxic to cells.
XX
SQ Sequence 558 BP; 149 A; 130 C; 124 G; 155 T; 0 other;
Query Match 71.8%; Score 536; DB 19; Length 558;
Best Local Similarity 99.1%; Pred. No. 1.3e-157;
Matches 539; Conservative 0; Mismatches 5; Indels 0; Caps 0;
QY 86 GTGAGAGTGAGAGATCTCAAAAGAAAGTGCCTTCTTCACTATTAACCTGCTCAAGC 145
Dd 3 gctgagagtgagagatctcaaaagaaagtgccttcttcaactgctcaactgctcaagc 62
QY 146 TCTGTAGCCTATGGGCTCCTATTGCTATTAATTCATGATTTGATACACAGACCTGGCTAAT 205
Dd 63 tcgtgagcctatgggctcctattgctatatactgctatcttgataccacagaccggtctaat 122
QY 206 GCAGACATATCCCTGCAGATGCTATTTCTCAGAGACACCTGGCATTTCTTCTCAGTACTGT 265
Dd 123 gcagacatctcctgcagatgctatcttcagagacacctgagattctctcagtaactggt 182
QY 266 GAAATTAACCTTGTGCTCCTCCTTGTGAGAACAGTTTGAAGCGCTACACATCATCTGG 325
Dd 183 gaaattaaccttgtgctcctccttgtgaagaaacagtttgagcgctacacagtaacttgy 242
QY 326 ATTGAGCTCCATGATCCCTGCATGATGATACCTACCAAGGAAGTGAAGTGAAGTGAAGC 385
Dd 243 attgagctccatgatccctgcatactgatactaccacaagaaagtgatggaagtgaagc 302
QY 386 AGTTCCATGCTGCTGACCTTCTATTAAGTGGAGAGAACCCCTCTATTTGCTGCTGACCGT 445
Dd 303 agttccaatgctgctgaccttctataactgagaggaagaaacctctatgtcgtcgacagt 362
QY 446 GCTTATTTGTGCAATTTTGTCTCAGAAATCAGTTTTCAGAAAGTGGAGAGATTTTAATTGT 505
Dd 363 gcttattgtgcaattttgtctcagaatcaggttttcagaagtggagatttlaattgt 422
QY 506 GAAATGAGCTTCCCTATATCTGCAAAATTCAGAGTCTAGGCACTTCTAATTTCAACAGC 565
Dd 423 gaaatgagcttccctatactcgaatcgaatcgaaggtcagggcagcttcaattcaacagc 482
QY 566 TTGAAATATTTATGAAAGCTCAGATGACCAAGAGCAAGTATGAGATTCTCAGAGAA 625
Dd 483 ttgaaatattatgaagctcacatgacagaaagaaagaaagatgtgagattcaactgaagaag 542
QY 626 AGCA 629
Dd 543 agca 546
RESULT 4
AAV30284
ID AAV30284 standard; DNA; 558 BP.
XX
XX AAV30284;
AC AAV30284;
XX
XX 25-SEP-1998 (first entry)
Dd
XX
DE INGAP coding sequence.
XX
```

Query Match	Best Local Similarity	71.8%	Score 536;	DB 19;	Length 558;
Matches 539;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;	
QY	86	GTGGAAGGTGAAGATATCAAAAGAAAGAACTGCCTTTCACGTATTAACCTGTCCTCAAGGC	145		
Db	3	gcgagatcccggaagaatattccaaagaagaactgctcttcttaacgataaacctgctctcaagc	62		
QY	146	TCTGTAGCCTTATGGTCTCTATTGCTATTTCAGTATTTGATACCAACAGACTGGTCTAAT	205		
Db	63	tctgtagcctatggtgtctctattgctattcactgattttgatataccaaagaccggtctaat	122		
QY	206	GCACACATATCTCGACACATGCATTTTCAGAGACACCGGCACTTTCCTCTCAGTACTGGT	265		
Db	123	gcagaaactatccctccaaatgcatcttcccaagaaaccctggaaattcttctccagatctggt	182		
QY	266	GAATTAACCTTCGTGTCTCCCTGTGTGAAGAACATTTTGACGGCCTTACAGTACATCTGG	325		
Db	183	gaattacctcttgctctcccttgtagaagaagtttgaacgcttacagatactctggt	242		
QY	326	ATTGGACTCCATGATCCCTCACATGTGTACTACCCAAAGCAAGTGGATGCAAGTGGAC	385		
Db	243	attggaactccatgtatccctcacatggtacatacccaacgaaagtgtgatlgaagtgaagc	302		
QY	386	AGTTTCAATGTGCGACCTTCTATTAACGGGGAGAGAACCCCTCTAATTTGCTGCTACCGT	445		
Db	303	agtttccaatgtgcgaccttctatacaacggagaaagaaaccctctatctgctgtaacgt	362		
QY	446	GGTATTTGTGCAGTTTGTCTCAGAAATCAGATTTTTCAGAAGTGGAGATTTTAATGT	505		
Db	363	ggtattctgtagtcttctgctccagaaatccaggtttctcgaagtgtgaagatatttaattgt	422		
QY	506	GAATATAGCTTCCCTATATCTGCAAAATTCAAAGGCTTAGGGCAGTTCTAATTTCAACAGC	565		

Db	423	gaaatgagcctcccatatctgcgaatccaagtcctaggcgagttctaatccaagc	483
Qy	566	TTGAAATATTTATGAGCTCATCATGACACAGCAAGCATGTGAGATTCTACCTCAGCAAG	625
Db	483	ttgaaatattatgaagctcacatgacagaagaagcaagtatgagattcaactcagaag	542
Qy	626	AGCA 629	
Db	543	agca 546	
RESULT 5			
ID	AAV58279	standard; cDNA: 763 BP.	
AC	AAV58279;		
DT	04-DEC-1998	(first entry)	
DE	Human pancreatitis-associated protein.		
XX			
KW	Human pancreatitis-associated protein; PAP-2; agonist; pancreatitis;		
KW	hyperplasia; hyperinsulinism; antagonist; tumour; oesophagus;		
KW	intestine; metastases; Crohn's disease; ulcerative colitis;		
KW	antibody; probe; PCR primer; amplification; hybridisation;		
KW	inhibitor; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	115..642	
FT		/*tag="a	
FT		/product="human PAP-2"	
XX			
PN	WC9841633-A1.		
XX			
PD	24-SEP-1998.		
XX			
PF	20-MAR-1998; 98WO-US05699.		
XX			
PR	20-MAR-1997; 97US-0822261.		
XX			
PA	(INCY-) INCYTE PHARM INC.		
XX			
PI	Goli SK, Hallman JL;		
DR	WPI; 1998-521222/44.		
DR	P-PSDB; AAW71682.		
PT	New pancreatitis-associated protein and related nucleic acid,		
PT	vectors, transformed cells - antibodies, agonists and antagonists,		
PT	for diagnosis, treatment and prevention of pancreatitis or other		
PT	pancreatic diseases, cancers, ulcerative colitis and Crohn's disease		
XX			
PS	Claim 5; Fig 1A-1B; 66pp; English.		
XX			
CC	This is the nucleotide sequence of the human pancreatitis-associated		
CC	protein (PAP-2), used in the method of the invention. The human		
CC	PAP-2, and its agonists are used to treat pancreatitis (particularly		
CC	to prevent or control associated bacterial infections) and other		
CC	pancreatic diseases such as hyperplasia and hyperinsulinism. Also		
CC	PAP-2 and its agonists/antagonists can be used to treat or prevent		
CC	tumours, e.g. of the pancreas, oesophagus or intestines, and/or		
CC	metastases, also Crohn's disease and ulcerative colitis. PAP-2 is		
CC	also used to raise antibodies and to screen libraries for		
CC	specific-binding agents. Antibodies are used for diagnosis or		
CC	monitoring of PAP-2-related diseases (in usual immunoassays), in		
CC	competitive drug screens and to isolate PAP-2 from natural sources.		
CC	PAP-2 derived probes or primers are used in standard amplification		
CC	or hybridisation tests to diagnose PAP-2-related diseases; to		
CC	identify related sequences; for genomic mapping and for screening for		
CC	specific inhibitors.		
XX			

SQ Sequence 763 BP, 182 A; 202 C; 197 G; 181 T; 1 other;

Query Match 40.8%; Score 304.8; DB 19; Length 763;
Best Local Similarity 67.1%; Pred. No. 2.8e-85;
Matches 432; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

OY 9 CAGTACCATGATGCTTCCATGACCCCTCTGAGATGCTGGATGCTTCTTCCG 68
DB 107 cagatcatatgtctcctccatgcccctgagctgctcgtatgcttctctgc 166
OY 69 TGAATCTCTTCTTGGGTGGAAGTGAAGATTCAAAAGAACTGCTTCTTCACTA 128
DB 167 tcatctcctgctgtaagctgtaagaaaccagaagaaactgctctccacg 226
OY 129 TACCTGTCCTTCAAGCTCTGAGCTTATGCTCTATTTGCTATTCACGATTTGATTC 188
DB 227 tcaagctgctcacaagctcacaagctcctgctcctgctcctgctcctgctc 286
OY 189 CACAGACCTGCTCTATGACAGAACTATCTGACATGCTTCTCAGACACTGTCAT 248
DB 287 caaatcctcgtatgctatgctatgctcgtcgtcgtcgtcgtcgtcgtcgtcgt 346
OY 249 TTTCTTCTAGTACGTGTAATTTACCTTCTGCTCTCTCTTGTGAAGAACTTTGACGG 308
DB 347 ctgtgctcagtggtgctgaggtacctctgctcctcctgctgaggtacgtlaaca 406
OY 309 CCTACAGTACATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 368
DB 407 gctactacatactcgtatgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 466
OY 369 GTGATGAGAGTGAAGAGCTTCAATGCTGCTGCTTCTATTAAGTGAAGAGAACTCT 428
DB 467 atggtatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 526
OY 429 CTATGCTGCTGACCGTGTATTTGCAAGTTTGTCTCAGAAATGAGTTTGAAGACT 488
DB 527 ccacatcctcaaccctgagccactgctgaggtcgtcgaagagcaagatctcgaagt 586
OY 489 GGAGAGATTTTAAATGTGAATGAGCTTCCCTATATCTGCAATTCAGAGCTCTAGCGCA 548
DB 587 ggaagaatataactgctgctgaagctaacctatgctcgtcgaagctgaagctgaagca 646
OY 549 GTTCTAATTTCAACAGCTTGAATAATTTATGAGCTCACTACATGAGAGCAAGTATG 608
DB 647 ggttggaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 706
OY 609 AGGATTCACCTGAGAGAGCAAGCTCTGCTTACACACCCACAC 652
DB 707 aagactcaaccctggaagaagaatattctcccaactgcccctacc 750

RESULT 6
AAZ34271
ID AAZ34271 standard; cDNA; 859 BP.

AAZ34271;

07-DEC-1999 (first entry)

Human PRO162 nucleotide sequence.

Human: PRO: EST: expressed sequence tag; PCR primer; hybridisation;
KW probe: blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.

OS Homo sapiens.

PN MO3946281-A2.

PD 16-SEP-1999.

PF 08-MAR-1999; 99WO-US05028.

XX 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0080349.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.

PR	15-MAY-1998;	98US--0085580.
PR	15-MAY-1998;	98US--0085582.
PR	15-MAY-1998;	98US--0085689.
PR	15-MAY-1998;	98US--0085697.
PR	15-MAY-1998;	98US--0085700.
PR	15-MAY-1998;	98US--0085704.
PR	18-MAY-1998;	98US--0086023.
PR	22-MAY-1998;	98US--0086392.
PR	22-MAY-1998;	98US--0086614.
PR	22-MAY-1998;	98US--0086430.
PR	22-MAY-1998;	98US--0086486.
PR	28-MAY-1998;	98US--0087098.
PR	28-MAY-1998;	98US--0087106.
PR	28-MAY-1998;	98US--0087208.
PR	30-JUL-1998;	98US--0094651.
PR	11-SEP-1998;	98US--0100038.
XX		
PA	(GETH) GENENTECH INC.	
PI	Wood WL, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	
XX		
DR	WPI; 1999-551358/46.	
DR	P-PADB; AAIV41735.	
XX		
PT	New secreted and transmembrane polypeptides and their polynucleotides,	
PT	useful for treating blood coagulation disorders, cancers and cellular	
PT	adhesion disorders -	
XX		
PS	Claim 2; Fig 1B2; 530bp; English.	
XX		
CC	The present invention describes secreted and transmembrane polypeptides	
CC	and their polynucleotides. The nucleotide sequences are useful as	
CC	sources of probes, primers, for chromosome mapping, and for generation	
CC	of antisense sequences. They can also be used to create transgenic	
CC	animals. The proteins can be used to treat a variety of diseases and	
CC	disorders, depending on their function. Diseases that may be treated	
CC	include blood coagulation disorders, cancers and cellular adhesion	
CC	disorders. They may also be used to raise antibodies. AAZ33691 to	
CC	AAZ34338, and AAIV41685 to AAIV1774 represent polynucleotide and	
CC	polypeptide sequence given in the exemplification of the present	
CC	invention.	
XX		
SQ	Sequence 859 BP; 223 A; 220 C; 193 G; 223 T; 0 other;	
Query Match	40.88; Score 304.8; DB 20; Length 859;	
Best Local Similarity	67.18; Pred. No. 2.9e-85;	
Matches 432; Conservative	0; Mismatches 212; Indels	0; Gaps
OY	9 CAGGTACCATATGATCGCTTCCATGCATGACCTCTGTGAGATGTCATTGGATGCGCTTCTGCC	68
DB		
DB	78 cagaacatactgctgcctcccatgacctgcccgcccaagtgtccttgatgtcgtcttccctgcgc	137
OY	69 TGATGTTCCCTTCTTGCGGTGAAGGTGAAGAATCTCAAAAAGAAACTGCCCTTTCACGTA	128
DB		
DB	138 tcaattcttcctgtcgaagttccaagttgaagaaccagaagaactgcctctccaagya	197
OY	129 TAACCTGTCCTCAAGGCTCTGTAGCCTATGGTGCTTATGCTATTCACCTGATTTTGATAC	188
DB		
DB	198 tcaggctgtccccaaaggtcccagaagcctaigtctccccctgactgtctgtttgtcac	257
OY	189 CACGACCTGGCTTAATNCAGAACATATCTCTCCAGATGCATTTTTCAGACACTCGGCAT	248
DB		
DB	258 caaatctcgtgatgtagatcgaatctggtctgcagaagcggccctctgtgaaaactcgtgt	317
OY	249 TTCTTTCACAGTAGTGGTGAATAATACCTTCTGTGTCTCCCTTGTGAAGACAGATTTCACGG	308
DB		
DB	318 ctgtgtccacgtggtggtggaagatcccttcgtctccctcctgtgtgagggacattagtaaca	377
OY	309 CCTTACGAGTACATCTGGATTTGGATGCTCAATGATNCCCTCAATGCTGATCTACACCAAGCAA	368
DB		
DB	378 gctactcatacatcttgatgtggtctccatgacacgacacacagggctctgaagctgagtgag	437

Qy	369	GTATGSAAGTGGAGAGAGCTTCATATGTCGGACCTCTATTACTGGAGAGAACCCCT	428
Db	438	atgatctggagctgagtagtaacacatgcatgcatgatactcttcacatgagagaaaaatccct	497
Qy	429	CTATTGCTGCTGACCGTGCTGTTATTTGTGCAGTTTGTCTCAGAAATCAGGTTTTCCAGAGT	488
Db	498	ccaccatcttaaccctctgacacgtctggagccctgtaagaagacagacgattctctgaagt	557
Qy	489	GGAGAGATTATTAATGTGCAAAATAGAGCTCCCTATTCTCAGAAATTCAGTAAGCTTAGGGCA	548
Db	558	ggaaagatcttaacatgcatgagcaaaagttaccctatgctcgaagttcaagacaaagctaaaggca	617
Qy	549	GTTCTAATTTTCAACAGCTTGAAAAATATTATGAAAGCTTCACATGCAAGCAAGAGCATATG	608
Db	618	ggttggaagctcagcagcctcagcttgctgctgacgtcatcatgacatgacagccagtggtg	677
Qy	609	AGGATTCACCTAGGAAGAAGCAGCTCTGCTCTACACACACCACACC	652
Db	678	aagactcacctctgaaagaaatattctctcccaaacctgcacctac	721

XX	RESULT	7
XX	AAC78569	
XX	ID	AAC78569 standard; cDNA; 859 BP.
XX	AC	
XX	AAC78569;	
XX	08-FEB-2001	(first entry)
XX	DT	
XX	DE	Human PRO162 (UNQ429) nucleotide sequence SEQ ID NO:451.
XX	KW	Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
XX	KM	expressed sequence tag; detection; cancer; ss.
XX	OS	Homo sapiens.
XX	PN	WO200053756-A2.
XX	PD	14-SEP-2000.
XX	PF	18-FEB-2000; 2000WO-US04341.
XX	PR	08-MAR-1999; 99WO-US05028.
XX	PR	12-MAR-1999; 99US-0123957.
XX	PR	29-MAR-1999; 99US-0126773.
XX	PR	21-APR-1999; 99US-0130232.
XX	PR	28-APR-1999; 99US-0131445.
XX	PR	14-MAY-1999; 99US-0134287.
XX	PR	23-JUN-1999; 99US-0141037.
XX	PR	26-JUL-1999; 99US-0145688.
XX	PR	29-OCT-1999; 99US-0162506.
XX	PR	30-NOV-1999; 99WO-US28313.
XX	PR	02-DEC-1999; 99WO-US28551.
XX	PR	02-DEC-1999; 99WO-US28565.
XX	PR	16-DEC-1999; 99WO-US30095.
XX	PR	30-DEC-1999; 99WO-US31243.
XX	PR	30-DEC-1999; 99WO-US31274.
XX	PR	05-JAN-2000; 2000WO-US00219.
XX	PR	06-JAN-2000; 2000WO-US00277.
XX	PR	06-JAN-2000; 2000WO-US00376.
XX	PA	(GETH) GENENTECH INC.
XX	PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX	PI	Perrina N, Filvaroff E, Fong S, Gao W, Gerber H, Gertlisen ME;
XX	PI	Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX	PI	Kiljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
XX	PI	Shelton DL, Stewart JA, Tumas D, Williams PM, Wood WI;
XX	WP	WPI: 2000-611443/58.
XX	DR	P-PSDB: AAB44311.
XX	Novel	PRO polypeptides and polynucleotides used in detection methods.

Db	275	ctgtgctcgaagtgaggcgccgaggagatccctcgtctccctccctcgtggtggaagacattggttaaca	334
Qy	309	CCCTACACAGTACATCTGGATTGGATTCGATCCATGATCCCTGCATCATGTGATACCTAACCGAA	368
Db	335	gctactacatgactctgattcggtctccatgaccccaacagagccagccgaatggag	394
Qy	369	GTGGATGTGAACTGAGGAGATTTCCAAATGCTGTACACTTTTATTAACCTGGAGAGAACCCCT	428
Db	395	aagctctggagctgagtagaagatgattgattgaattcattgcaatgaggagaatccct	454
Qy	429	CTATTGCTGCTGACCCGTGTATTGTGTCACATTTTGTCTCAGAAATACAGSTTTTCAGAAAT	488
Db	455	ccacacatcctcaagcccccgcacactctgctgagcctctgcggaagacacagatcttcgaggt	514
Qy	489	GGAGAGATTTTAAATTTGTGAAATAGCTTCCATATATCTGACAAATTCAGAGTCTAGGGCA	548
Db	515	ggaagaattactgaactgtaatgtagtgaagttaccatctatctgcgaagtctactgattgta	574
Qy	549	GTTCTAATTTTCACACGCTTGCAAAATATATATGAAAGCTCACATGTGACAGAGAACAGTATG	608
Db	575	ggaggggaagtcagcagccctgctgttctgctgacacatccatcatgagcatgagaccagtg	634
Qy	609	AGGATTCATCTACGAGAGAGACAGCTCTGCTACACACCCACACACAAATTCCTTAT	663
Db	635	aggactcacctcgtggaagagatatattgcttaattcccccacactgacacactcat	689
RESULT 9			
XX	ACCT7777	AACCT7777 standard; cDNA, 940 BP.	
XX	ACCT7777;		
XX	08-FEB-2001	(first entry)	
XX	Human cancer associated gene sequence SEQ ID NO:171.		
XX	DE	Human: cancer associated gene; cancer antigen; detection; cancer;	
XX	KW	diagnosis; cytostatic; proliferative; vulnery; immunomodulator;	
XX	KW	antidiabetic; antistaphylococcal; antineoplastic; antithrombotic; antiviral;	
XX	KW	antiinflammatory; antihypertensive; antitubercular; antibacterial; cardiac;	
XX	KW	dermatological; neuroprotective; thrombolytic; coagulant; noctropic;	
XX	KW	vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;	
XX	KW	immune disorder; haematopoietic cell disorder; autoimmune disorder;	
XX	KW	hemostatic reaction; graft versus host disease; organ rejection;	
XX	KW	hemostatic; thrombolytic; cardiovascular disorder; infection;	
XX	KW	neurological disease; drug screening; ss.	
XX	OS	Homo sapiens.	
XX	XX	WO200055350-A1.	
XX	PN	21-SEP-2000.	
XX	PD	08-MAR-2000; 2000MO-US05882.	
XX	PF	12-MAR-1999; 99US-0124270.	
XX	PR	(HUMA-) HUMAN GENOME SCI INC.	
XX	PA	Rosen CA, Ruben SM;	
XX	PI	WPI; 2000-587533/55.	
XX	DR	P-PSDB; AAB43568.	
XX	DR	Novel isolated nucleic acids comprising sequences encoding peptides	
XX	PT	useful for treating or diagnosing e.g. cancer -	
XX	XX	Claim 1; Page 750; 2352pp; English.	
XX	PS	AACCT7607 to AACCT8448 encode the human cancer associated proteins given	
XX	CC	in AAB43398 to AAB44239. The proteins can have activities based on the	
XX	CC	tissues and cells the genes are expressed in. Example of activities	

CC Include: cytostatic; proliferative; vunerary; immunomodulator;
CC antidiabetic; antiasthmatic; antithrombotic; antiarrhythmic;
CC antiinflammatory; antihypertoid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiac; thrombolytic; Coagulant;
CC neotropic; vasotropic; antipruritic and antilangogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB84240 represent sequences used in the exemplification of
CC the present invention.

Query Match	39.7%;	Score 296.6;	DB 21;	Length 940;
Best Local Similarity	65.8%;	Pred. No. 1.1e-82;		
Matches 431; Conservative	0;	Mismatches 224;	Indels 0;	Gaps 0;

OY	9	CAGGATACCAATGATGGCTTCCCATGACCCTCTGTAGAGATTGCTTGGAATGCCTTCCTGCC	68
Db	70	cagacatactgctgcctcccaagcctcgccagtgatctctggatgctgcttccctgc	129
OY	69	TGATGTTCCTTTCTTGGGTGGAAAGGTGAAGAATCTCATAAAGAAACTGCCCTTTCACGTA	128
Db	130	tcatgtcgtctcagtltccaagtltagaagaaccacaagggaattgccttcctgcacga	189
OY	129	TAACTGTCTCAAAGGCTCTTAGCGCTTAGGCTTATGGCTCTATTGCTATTCACATGATTTGATAC	188
Db	130	tccgctgtgcccaaagctccaaagcctlaagctcccaactgcacatgacctgttgtttgtcac	249
OY	189	CACAGACCTGTGCTTATGCTAGCACAGACATCTCCGCAGATGCATTTTTCAGAGACACTGCAT	248
Db	250	caaatccctgcagacagatgcagatctgctcctgcagaaagcgccctctgaaacctggtgt	309
OY	249	TTCTCTCTCAGTACTGTGGTAATTAATTAACCTTCGTGCTCTCCCTTGTGAAGAACAATTTGACGG	308
Db	310	ctgtgctcagtgaggctgaaggatccctctgtctcctcctgtgtgaagacatltgtlaaca	369
OY	309	CCTACACGTATACATCTGGAATTGGACTTCATGATCCCTCACATGTGTCACATCCCAACGNA	368
Db	370	gctactcatacgtctcgtgatltggctcccatgaccaccaacaggacacgcagccccaatltag	429
OY	369	GTCGATGGAAGTGGACGACTTCCAATGTGCTGACCTTCTATATCTGGGAGAGAACCCCT	428
Db	430	aaggtctggagctgtagtagcagtgatctgtaactctltbcacayggagagaaatccct	489
OY	429	CTATTGCTGCGACCGTGSTTATTTGTGGAGTTTGTTCAGAAAATCAGGTTTTCAAGAT	488
Db	480	ccaacatctcaagcccggccacgctvgcgagccctctgagaaagacaagatcttcgaggt	549
OY	489	GGAGAGATTTAATTGTGAAAAATGAGCTTCCCTATATCTGCAAAATTCAGAGCTTAGGGCA	548
Db	550	ggaagaattataactgatatltgaggttacctctaactgtctgcaagtlcaactgactvagta	609
OY	549	GTTCTAATTTTCACAGCTTTGAAAATATATATGAAAGTCCACATGACACAGGAAGCAAGTATG	608
Db	610	ggaagggaagctacagcgcctgtgttgtgtgcacatcatctggcagtagaacgcgtgtg	669
OY	609	AGGATTCTACAGAGAGAGCAAGCTCTGCCATACACACCACACACCAATTCOCCTTA	663
Db	670	aggactcaacctgbaagagaaatatctgcttaattccccaacctfgacacacctcat	724

OY 369 GTGATGGAAGTGGACGCTTCCAAATGTCGACCTTCTATTAACCTGGAGAGAACCCCT 428
11 11111111 11 1111 11 11 11111111 1111
Db 395 aaggttgggaatgtagtagcagtgatgtagtaattacttgcatgtaggaagaatccct 454
OY 429 CTATTGCTGCTGACCGTGTTATTTGTGCAAGTTTGTCTCAAAATCAGGTTTTCAGAGT 488
11 11 11 11 11 1111 1111 11 11 11111111
Db 455 ccacatctcaagcccccgcacgtgagcagccttcgagaagcagcatttcgaagt 514
OY 489 GGAGAGATTTTAAATTTGAAATAGAGCTTCCCTATTTATCTGAAA-TTCAGGCTTAGGGC 547
111 11111 111 111 111111111111 1111 1111 11
Db 515 ggaagaattataactgtatgtgaggttacctatgtctgcaaaagttcaactgactagtgc 574
OY 548 AGTTCTAATTTCAACAGCTTGAATAATTTATGAAGCTTCACATGAGCAAGAGCAAGTAT 607
11 111 1111 11 11 1111 11 11 1111 11
Db 575 aggaagggaagtcagcagcgtgtgtgtgtgcaactcatcatgagcagcagtggt 634
OY 608 GAGATTCACACGAGAGAGAGAGAGCTGCTACACACCCACCAATTCCTTAT 663
11111 1111 1111111 11 1111 11 1111 11
Db 635 gagagctacacctggaagaataatctgcttaattcccccaacctgagccacctcat 690

RESULT 13

AAx26126 standard; DNA; 781 BP.
ID AAX26126

XX AAX26126;

XX 20-MAY-1999 (first entry)

XX Reg-2 protein encoding DNA.

XX Reg-2 protein encoding DNA.

KW Reg-2; Schwann cell mitogen; repair; regenerate; neuronal cell; tissue;

XX Rattus sp.

XX GB2329335-A.

XX 24-MAR-1999.

XX 16-SEP-1998; 98GB-0020193.

XX 17-SEP-1997; 97GB-0019796.

XX (MED1-) MEDICAL RES COUNCIL.

XX Hunt SP, Livsey EJ;

XX WPI; 1999-156299/14.

XX P-PSDB; AAW95089.

XX Use of a protein (Reg-2) to manufacture a Schwann cell mitogen. - to

XX repair and/or regenerate neuronal cells or tissue, either in vivo, or

XX or in vitro and then introduced into subject

XX Disclosure; Page 24-25; 33pp; English.

XX The invention relates to the use of a protein (Reg-2) or its variant,

XX derivative or homologue to manufacture a Schwann cell mitogen. Reg-2 is

XX used to repair and/or regenerate neuronal cells or tissue. Neuronal cells

XX or tissue may be repaired and/or regenerated either in vivo, or in vitro

XX and then introduced into a subject. Reg-2 unlike known Schwann cell

XX mitogens e.g. glial growth factors/neuregulins, are upregulated during

XX regeneration. The present sequence represents a DNA encoding the Reg-2

XX protein.

XX Sequence 781 BP; 221 A; 181 C; 177 G; 202 T; 0 other;

XX Query Match 38.48; Score 286.8; DB 20; Length 781;

XX Best Local Similarity 65.48; Pred. No. 1.2e-79;

XX Matches 420; Conservative 0; Mismatches 222; Indels 0; Gaps 0;

OY 5 AAGACAGTACCATGANGCTTCCCATGACCTCTGTAGAGTCTTGATGCTGCTTCC 64
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 50 atgagagtaataatgatgcatcgtcgtcctcccaagcagtcgtcctgatgctgctcc 109
OY 65 TGCCGTGATGTTCCCTTCTTCTGCGTGGAGGTGAAGATTCAGAAATTCAGCTTCTTCA 124
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 110 tgcctgagctcttataccaaggtgcaagaaagacttcggaagaaataacccttcga 169
OY 125 CGTAAACCTGCTCAAGGCTCTGTAGCTCATGAGTCCCTATTCCTATTCAGTATTG 184
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 170 cgcattagttccccaaggtctccaggcataatgctcctcctatgacctgttllag 229
OY 185 ATACACAGACCTGGTCAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAG 244
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 220 ataccacagacctgtgttgatgcaagaactgctgcagcaagagagaccctgaagacactt 289
OY 245 GCATTTCTTCTCAGTACTGCTGGAATTAATTCCTGCTGCTGCTGCTGCTGCTGCTG 304
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 290 gtaactgtgctcaatgtagctgaagcttcaattcttgatcattcattgtaagaacactgga 349
OY 305 ACGGCTACGATCATGCTGATGGAATTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTG 364
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 350 aacagctacccaataatgactgtagtgcagctccacccactctgtgtgaggaacccaat 409
OY 365 GGAAGTGATGGAAGTGGAGCAGTTCGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 410 ggaagtgtagtggagtgtagtgaatacaatgacataatgataatgtaactgtaggaagac 469
OY 425 CCTCTATTGCTGCTGACCGTGTTATTGTCAGTTTGTCTCAGAAATTCAGGTTTTCAG 484
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 470 ccacttactgctttagaacccgcgagcttctgtgcagctgtgcaagatcttccgatttcta 529
OY 485 AAGTGACAGATTTTAAATTTGAAATAGAGCTTCCCTATTCGAAATTCGAAGTCTAG 544
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 530 agatggagagataccaacgtggaagtggaagtggaagtggaagtggaagtggaagtgga 589
OY 545 GGCAGTTCTAATTTCAACAGCTTGAATAATTTATGAACTGACATGACAGAGAGCAAG 604
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 590 aataccagagacagaacaagctttagtltgtccgtgaagcaatcctgtgcaaggggcaaaa 649
OY 605 TATGAGATTGCTCAGAGAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 646
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 650 tatgaagacttgcgtlaagaaagtgatctatctatctacagctcc 691

RESULT 14

AAx75486 standard; DNA; 781 BP.
ID AAx75486

XX AAx75486;

XX 15-JAN-2001 (first entry)

XX DNA encoding a rat Reg-2 polypeptide.

XX Schwann cell mitogen; Reg-2; neuronal cell regeneration; motor neuron;

XX neuron-glia interaction; ss.

XX Rattus sp.

XX Key Location/Qualifiers

XX CDS 62..557

XX FT //tag= a

XX FT /product= "Reg-2"

XX GB2347931-A.

XX 20-SEP-2000.

XX 02-FEB-2000; 2000GB-0002424.

XX 17-SEP-1997; 97GB-0019796.

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PR 16-SEP-1998; 98GB-0020193.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Livesey FJ, Hunt SP;
XX
XX MPI; 2000-567204/53.
XX
XX P-PSDB; AAB18614.
XX
XX New Schwann cell mitogen (known as Reg-2), useful for repair and
XX regeneration of neuronal cells and tissue, is upregulated during
XX neuronal regeneration.
XX
XX Disclosure; Page 24; 32pp; English.
XX
XX The present sequence encodes a Schwann cell mitogen, known as Reg-2.
XX Reg-2 can be upregulated during regeneration of neuronal cells and
XX tissue. Reg-2 is an essential component in neuron-glia interaction
XX that underlies development and regeneration of mammalian motor
XX neurons. It is a 16 kDa protein. Reg-2 is used to affect development
XX of neuronal cells and tissue, especially for promoting their repair
XX and regeneration, particularly of motor cells in adult humans.
XX
XX Sequence 781 BP; 221 A; 181 C; 177 G; 202 T; 0 other;
SQ
Query Match 38.4%; Score 286.8; DB 21; Length 781;
Best Local Similarity 65.4%; Pred. NO.1.2e-79;
Matches 420; Conservative 0; Mismatches 222; Indels 0; Gaps 0;
0;
QY 5 AAGACAGGTACGATGATCTTCCATGACCCCTGTAGATGCTTGATGCTGCTTCC 64
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 50 atgagagtaataatgtatgcatgcttgctccagctatgctgctgctgctc 109
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 65 TGCCTGATGCTCTTCTTTGGGTGGAAGTGGAAGATCTCAAAAAGAACCTCTTCA 124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 110 tgcctgatgctctatcatcagctgcaagagaaactccgaagaaataacccctcgca 169
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 125 CGATATACCTGCTCCTCAAGGCTGATGAGGCTGATGCTGATGCTGATGCTGATGCTG 184
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 170 cgaatagctgcccacaagctcccaagcatatgctcccaagctgctgctgctcag 229
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 185 ATACACAGACCTGCTCTATGATGAGACATACCTGACGATGATCTCTAGACACCTG 244
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 230 ataccacagaccctggttgcagaaactgctgcccagaagagactcgtgaagacac 289
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 245 GCATTTCTTCTCAGTACTGCTGAAATTAACCTGCTGCTCCCTTGGAAGAACAGTTTG 304
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 290 gtaatgctgctcatgactgaaagctcatcttgcacatccatgctcaagaaacatgga 349
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 305 ACGGCTTACAGACATGCTGATGAGCTGACATGATGCTGACATGCTGATGCTGATGCTG 364
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 350 aacagctacacatacatcagatgactgacatgacacccactgctgctgagacccaat 409
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 365 GGAAGTGGATGAGAGTGGAGACATTCATATGCTGACCTTCTATACCTGGAGAGGAGAC 424
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 410 gggagtgagatggagagtgagtaacaatgacataatgataatgtaactgaggaggaac 469
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 425 CCTCTATTGCTCTGACCTGCTGATTTGTGACAGTTTGTCTCAAGAAATCAGGTTTTCAG 484
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 470 ccaatctactctcttagaccgcgagatctctgagacgttgcagaatctcttctgatttcta 529
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 485 AATGAGAGATTTTATTTGTAATGAGCTTCCATATTCGCAATTCAGAGCTTAG 544
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 530 agatgagagatacatcacaatgagagtgagtgccctacagctcgcaaatltaacagttaa 589
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 545 GCGAGTTCTTATTTCACACCTTGAAATATTTATGAAGCTACATGAGACAGAGAGCAAG 604
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 590 aattaccagagacagcaacagctttagtttgcctgaaagacatccgtcaagggcaca 649
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 605 TATGAGATTTCACTCAGAGAGACCAAGCTCTGCTTACACAC 646
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 650 tatgaagacttgctgtagaagaaagtatctatctacagctc 691
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 15
AA014621
ID AA014621 standard; cDNA; 793 BP.
XX
XX AC AA014621;
XX
XX 29-JAN-1992 (first entry)
XX
XX DE Fragment SI encoding rat pancreatitis associated protein.
XX
XX hPAP; pancreas; imaging; ss.
XX
XX Rattus.
XX
XX OS
XX
XX Key Location/Qualifiers
XX sig_peptide 61..139
XX FT /tag- a
XX FT 140..613
XX FT mat_peptide /tag- b
XX FT /product- PAP
XX
XX WO9116428-A.
XX
XX PN
XX
XX PD 31-OCT-1991.
XX
XX PF 18-APR-1991; 91WO-PK00323.
XX
XX PR 20-APR-1990; 90PR-0005062.
XX
XX PA (INRM ) INSERM INST NAT SANTE.
XX
XX PI Iovanna JL, Keim V, Dagron JC;
XX
XX DR MPI; 1991-339816/46.
XX
XX P-PSDB; AAR14797.
XX
XX PT cDNA fragment of human pancreatitis associated protein -
XX produced by genetic engineering, and the corresponding antibody,
XX for use in the diagnosis of pancreatitis
XX
XX PS Claim 8; Page 30; 49pp; French.
XX
XX CC The cDNA fragment SI encodes the rat PAP. It
XX was isolated from a rat pancreatic cDNA library using antibodies
XX against rat PAP. The cDNA was used as a probe to screen a human
XX pancreatic cDNA library to identify human PAP sequences.
XX
XX SQ Sequence 793 BP; 232 A; 181 C; 177 G; 203 T; 0 other;
SQ
Query Match 37.3%; Score 279; DB 12; Length 793;
Best Local Similarity 65.6%; Pred. NO.3.3e-77;
Matches 422; Conservative 0; Mismatches 220; Indels 1; Gaps 1;
1;
QY 5 AAGACGTAACATGATGCTTCCATGACCCCTGTAGATGCTTGATGCTGCTTCC 64
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 50 atgagagtaataatgtatgcatgcttgctccagctatgctgctgctgctc 109
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 65 TGCCTGATGCTCTTCTTTGGGTGGAAGTGGAAGATCTCAAAAAGAACCTCTTCA 124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 110 tgcctgatgctctatcatcagctgcaagagaaactcgcgaagaaataacccctcgca 169
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 125 CGTATACCTGCTCCTCAAGGCTGATGAGGCTGATGCTGATGCTGATGCTGATGCTG 184
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 170 cgaatagctgcccacaagctcccaagcatatgctcctactgctatgcccgtttcag 229
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 185 ATACACAGACCTGCTCTATGATGAGACATACCTGACGATGATCTCTAGACACCTG 244
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 230 ataccacagaccctggttgcagaaactgctgcccagaagagactcgtgaagacac 289
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 245 GCATTTCTTCTCAGTACTGCTGAAATTAACCTGCTGCTCCCTTGGAAGAACAGTTTG 304
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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